

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:37:44 ; Search time 47 Seconds  
(without alignments)  
156.556 Million cell updates/sec

Title: US-10-785-230-5  
Perfect score: 463  
Sequence: 1 MNAKVVVVLVLVLTALCLSD.....VCIDPKLKWIQYILEKALNK 89

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	463	100.0	89	1	US-08-323-084A-1	Sequence 1, Appli
2	463	100.0	89	1	US-08-674-008-1	Sequence 1, Appli
3	463	100.0	89	2	US-09-461-912A-46	Sequence 46, Appl
4	463	100.0	89	2	US-09-175-713-1	Sequence 1, Appli
5	463	100.0	89	2	US-09-647-501-4	Sequence 4, Appli
6	463	100.0	93	1	US-08-323-084A-5	Sequence 5, Appli
7	463	100.0	93	1	US-08-674-008-5	Sequence 5, Appli
8	463	100.0	93	2	US-09-919-497-95	Sequence 95, Appl
9	463	100.0	93	2	US-09-949-016-5967	Sequence 5967, Ap
10	463	100.0	93	2	US-09-144-838-7	Sequence 7, Appli
11	463	100.0	93	2	US-09-175-713-2	Sequence 2, Appli

12	463	100.0	119	2	US-09-949-016-8247	Sequence 8247, Ap
13	463	100.0	166	2	US-09-646-028-5	Sequence 5, Appli
14	463	100.0	328	2	US-08-808-720-1	Sequence 1, Appli
15	463	100.0	328	2	US-09-467-638-1	Sequence 1, Appli
16	442	95.5	89	1	US-08-181-556-2	Sequence 2, Appli
17	442	95.5	93	2	US-09-312-283C-421	Sequence 421, App
18	440	95.0	326	2	US-08-808-720-3	Sequence 3, Appli
19	440	95.0	326	2	US-09-467-638-3	Sequence 3, Appli
20	377	81.4	177	2	US-09-646-028-54	Sequence 54, Appl
21	377	81.4	339	2	US-09-646-028-55	Sequence 55, Appl
22	369	79.7	90	2	US-09-175-713-12	Sequence 12, Appl
23	369	79.7	94	2	US-09-175-713-13	Sequence 13, Appl
24	365	78.8	68	2	US-09-175-713-14	Sequence 14, Appl
25	365	78.8	69	2	US-09-175-713-10	Sequence 10, Appl
26	365	78.8	72	2	US-09-175-713-15	Sequence 15, Appl
27	365	78.8	72	2	US-09-646-193-7	Sequence 7, Appli
28	365	78.8	72	2	US-09-646-192-7	Sequence 7, Appli
29	365	78.8	73	2	US-09-175-713-11	Sequence 11, Appl
30	360	77.8	67	2	US-09-144-838-8	Sequence 8, Appli
31	360	77.8	67	2	US-09-144-838-23	Sequence 23, Appl
32	360	77.8	67	2	US-09-646-193-6	Sequence 6, Appli
33	360	77.8	67	2	US-09-646-192-6	Sequence 6, Appli
34	342.5	74.0	66	2	US-09-144-838-27	Sequence 27, Appl
35	321	69.3	68	2	US-09-144-838-51	Sequence 51, Appl
36	309	66.7	68	2	US-09-144-838-24	Sequence 24, Appl
37	306	66.1	67	2	US-09-144-838-25	Sequence 25, Appl
38	304	65.7	67	2	US-09-144-838-47	Sequence 47, Appl
39	291.5	63.0	67	2	US-09-144-838-28	Sequence 28, Appl
40	270	58.3	69	2	US-09-144-838-52	Sequence 52, Appl
41	268.5	58.0	66	2	US-09-144-838-29	Sequence 29, Appl
42	267	57.7	68	2	US-09-144-838-53	Sequence 53, Appl
43	255	55.1	68	2	US-09-144-838-26	Sequence 26, Appl
44	253	54.6	68	2	US-09-144-838-48	Sequence 48, Appl
45	250	54.0	67	2	US-09-144-838-49	Sequence 49, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-323-084A-1

; Sequence 1, Application US/08323084A

; Patent No. 5563048

; GENERAL INFORMATION:

; APPLICANT: HONJO, TASUKU

; APPLICANT: SHIROZU, MICHIO

; APPLICANT: TADA, HIDEAKI

; TITLE OF INVENTION: No. 5563048e1 Polypeptides and DNAs encoding them

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

; STREET: 2100 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20037-3202

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,084A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-323-084A-1

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Query Match          100.0%; Score 463; DB 1; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.8e-52;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

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## RESULT 2

US-08-674-008-1

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; Sequence 1, Application US/08674008
; Patent No. 5756084
; GENERAL INFORMATION:
; APPLICANT: HONJO, Tasuku
; APPLICANT: SHIROZU, Michio
; APPLICANT: TADA, Hideaki
; TITLE OF INVENTION: HUMAN STROMAL DERIVED
; TITLE OF INVENTION: FACTOR 1` AND 1 (As Amended)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/674,008
;   FILING DATE:  1-JUL-1996
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/323,084
;   FILING DATE:  14-OCT-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  JP 280505/1993
;   FILING DATE:  14-OCT-1993
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (202)293-7060
;   TELEFAX:  (202)293-7860
;   TELEX:  6491103
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  89 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-674-008-1

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Query Match          100.0%;  Score 463;  DB 1;  Length 89;
Best Local Similarity 100.0%;  Pred. No. 9.8e-52;
Matches   89;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
        ||||||||||||||||||||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

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# RESULT 3

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US-09-461-912A-46
; Sequence 46, Application US/09461912A
; Patent No. 6709855
; GENERAL INFORMATION:
; APPLICANT:  Stanton, Lawrence A.
; APPLICANT:  White, R. Tyler
; APPLICANT:  Damm, Deborah L.
; APPLICANT:  Lewicki, John A.
; TITLE OF INVENTION:  Methods for detection and use of
; TITLE OF INVENTION:  differentially expressed genes in disease states
; FILE REFERENCE:  SCIOS.011A
; CURRENT APPLICATION NUMBER:  US/09/461,912A
; CURRENT FILING DATE:  1999-12-15
; PRIOR APPLICATION NUMBER:  US 60/113,008
; PRIOR FILING DATE:  1998-12-18
; NUMBER OF SEQ ID NOS:  48
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 46
;   LENGTH:  89

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;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-461-912A-46
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Query Match 100.0%; Score 463; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 9.8e-52;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MNAKVVVVVLVLVTALCLSDGKPVSLSYRCP RFFESHVARANVKHLKILNTPNCALQIV 60
        |||||||

Qy      61 ARLKNNNRQVCIDPKLKWIEYLEKALNK 89
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Db      61 ARLKNNNRQVCIDPKLKWIEYLEKALNK 89

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## RESULT 4

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US-09-175-713-1
; Sequence 1, Application US/09175713
; Patent No. 6852508
; GENERAL INFORMATION:
; APPLICANT: Herrmann, Stephen H.
; APPLICANT: Lu, Zhijian
; APPLICANT: McCoy, John M.
; APPLICANT: Swanberg, Stephen L.
; APPLICANT: Walker, Bruce
; APPLICANT: Yang, Otto
; TITLE OF INVENTION: CHEMOKINES WITH AMINO-TERMINAL MODIFICATIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/175,713
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; STRANDEDNESS:

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; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-175-713-1

Query Match 100.0%; Score 463; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 9.8e-52;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
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Db 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
|  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 5

US-09-647-501-4  
; Sequence 4, Application US/09647501  
; Patent No. 6863887  
; GENERAL INFORMATION:  
; APPLICANT: No. 6863887thwest Biotherapeutics, Inc.  
; APPLICANT: Murphy, Gerald P.  
; APPLICANT: Boynton, Alton L.  
; APPLICANT: Sehgal, Anil  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED ON THE  
; TITLE OF INVENTION: ROLE OF THE CXCR-4 GENE IN TUMORIGENESIS  
; FILE REFERENCE: 20093-000600PC  
; CURRENT APPLICATION NUMBER: US/09/647,501  
; CURRENT FILING DATE: 2000-09-24  
; PRIOR APPLICATION NUMBER: 60/079,916  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/104,656  
; PRIOR FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-647-501-4

Query Match 100.0%; Score 463; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 9.8e-52;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
|  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 6

US-08-323-084A-5  
; Sequence 5, Application US/08323084A  
; Patent No. 5563048  
; GENERAL INFORMATION:  
; APPLICANT: HONJO, TASUKU  
; APPLICANT: SHIROZU, MICHIO  
; APPLICANT: TADA, HIDEAKI  
; TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20037-3202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/323,084A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 280505/1993  
; FILING DATE: 14-OCT-1993  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)293-7060  
; TELEFAX: (202)293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 93 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-323-084A-5

Query Match 100.0%; Score 463; DB 1; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1e-51;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
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Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 7  
US-08-674-008-5  
; Sequence 5, Application US/08674008  
; Patent No. 5756084

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; GENERAL INFORMATION:
; APPLICANT: HONJO, Tasuku
; APPLICANT: SHIROZU, Michio
; APPLICANT: TADA, Hideaki
; TITLE OF INVENTION: HUMAN STROMAL DERIVED
; TITLE OF INVENTION: FACTOR 1` AND 1 (As Amended)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,008
; FILING DATE: 1-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,084
; FILING DATE: 14-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-674-008-5

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Query Match          100.0%; Score 463; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches    89; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

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Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
        ||||||||||||||||||||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

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RESULT 8
US-09-919-497-95
; Sequence 95, Application US/09919497

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; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-95
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Query Match          100.0%; Score 463; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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RESULT 9

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US-09-949-016-5967
; Sequence 5967, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5967
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5967
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Query Match          100.0%; Score 463; DB 2; Length 93;
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Best Local Similarity 100.0%; Pred. No. 1e-51;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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RESULT 10

US-09-144-838-7

; Sequence 7, Application US/09144838A  
; Patent No. 6844161  
; GENERAL INFORMATION:  
; APPLICANT: Siani, Michael A.  
; APPLICANT: Wilken, Jill  
; APPLICANT: Simon, Reyna  
; APPLICANT: Kent, Stephen B.H.  
; TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation  
; FILE REFERENCE: GRFN-020/01US  
; CURRENT APPLICATION NUMBER: US/09/144,838A  
; CURRENT FILING DATE: 1998-08-31  
; EARLIER APPLICATION NUMBER: US 60/057,620  
; EARLIER FILING DATE: 1997-09-04  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 93  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-144-838-7

Query Match 100.0%; Score 463; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1e-51;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
          |||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 11

US-09-175-713-2

; Sequence 2, Application US/09175713  
; Patent No. 6852508  
; GENERAL INFORMATION:  
; APPLICANT: Herrmann, Stephen H.  
; APPLICANT: Lu, Zhijian

```

; APPLICANT: McCoy, John M.
; APPLICANT: Swanberg, Stephen L.
; APPLICANT: Walker, Bruce
; APPLICANT: Yang, Otto
; TITLE OF INVENTION: CHEMOKINES WITH AMINO-TERMINAL MODIFICATIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/175,713
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-175-713-2

```

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Query Match          100.0%; Score 463; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCP RFFESHVARANVKHLKILNTPNCALQIV 60
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Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCP RFFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
        ||||||||||||||||||||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

```

# RESULT 12

```

US-09-949-016-8247
; Sequence 8247, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```

```
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8247
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8247
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Query Match          100.0%; Score 463; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.4e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
          |||
Db      27 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 86
          |||

Qy      61 ARLKNNNRQVCIDPKLKWIEYLEKALNK 89
          |||
Db      87 ARLKNNNRQVCIDPKLKWIEYLEKALNK 115
          |||
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# RESULT 13

```
US-09-646-028-5
; Sequence 5, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER
VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic
construct
US-09-646-028-5
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Query Match 100.0%; Score 463; DB 2; Length 166;  
Best Local Similarity 100.0%; Pred. No. 2.2e-51;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 14

; Patent No. 6100387

APPLICANT: Swanberg, Stephen

; TITLE OF INVENTION: CHEMOKINE DOMAINS

CORRESPONDENCE ADDRESS:

STREET: 87 CambridgePark

STATE: MA

ZIP: 02140

```

:      MEDIUM TYPE:  Floppy disk

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:      COMPUTER:      IBM PC COMPACT/PC
:      OPERATING SYSTEM:  PC-DOS/MS-DOS

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```

: CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/808,720

;  
FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

; NAME: Sprunger, Suzanne

REGISTRATION NUMBER: P-41,323

REFERENCE/DOCKET NUMBER: GI5291

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8284

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 328 amino acids

```
;      TYPE:  amino acid
```

; STRANDEDNESS:

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;      TOPOLOGY:  linear
```

; MOLECULE TYPE: protein

US-08-808-720-1

Query Match 100.0%; Score 463; DB 2; Length 328;



Query Match 100.0%; Score 463; DB 2; Length 328;  
Best Local Similarity 100.0%; Pred. No. 5.1e-51;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
          ||||||||||||||||||||||||||||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

Search completed: April 26, 2006, 02:39:05  
Job time : 47 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2006, 02:30:38 ; Search time 225 Seconds  
(without alignments)  
279.076 Million cell updates/sec

Title: US-10-785-230-5  
Perfect score: 463  
Sequence: 1 MNAKVVVVLVLVLTALCLSD.....VCIDPKLKWIQEYLEKALNK 89

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	463	100.0	89	2 Q6ICW0_HUMAN	Q6icw0 homo sapien
2	463	100.0	92	2 Q9H554_HUMAN	Q9h554 homo sapien
3	463	100.0	93	1 SDF1_HUMAN	P48061 homo sapien
4	463	100.0	119	2 Q5IT36_HUMAN	Q5it36 homo sapien
5	455	98.3	89	2 Q8HYP0_MACMU	Q8hyp0 macaca mula
6	447	96.5	93	2 Q5R8M6_PONPY	Q5r8m6 pongo pygma
7	445	96.1	89	2 Q54AJ3_FELCA	Q54aj3 felis silve
8	445	96.1	93	1 SDF1_FELCA	O62657 felis silve
9	442	95.5	89	1 SDF1_MOUSE	P40224 mus musculu
10	442	95.5	89	2 Q543V6_MOUSE	Q543v6 mus musculu
11	442	95.5	93	2 Q4FJL5_MOUSE	Q4fjl5 mus musculu
12	442	95.5	137	2 Q80ZW4_MOUSE	Q80zw4 mus musculu
13	437	94.4	89	2 Q5XNN9_CANFA	Q5xnn9 canis famil
14	435	94.0	89	2 Q9QZD1_RAT	Q9qzd1 rattus norv
15	435	94.0	119	2 Q80YV8_RAT	Q80yv8 rattus norv



16	428	92.4	116	2	Q6EKW4_PIG	Q6ekw4	sus	scrofa
17	359	77.5	89	2	Q6T7C0_CHICK	Q6t7c0	gallus	gall
18	359	77.5	131	2	Q6T7B9_CHICK	Q6t7b9	gallus	gall
19	341	73.7	93	2	Q5EBF6_XENTR	Q5ebf6	xenopus	tro
20	341	73.7	94	2	Q8UUJ9_XENLA	Q8uuj9	xenopus	lae
21	225.5	48.7	99	2	Q4QTK3 ICTPU	Q4qtk3	ictalurus	p
22	224.5	48.5	99	2	Q8AV10_BRARE	Q8av10	brachydanio	
23	220.5	47.6	97	2	Q6V9B5_BRARE	Q6v9b5	brachydanio	
24	209.5	45.2	97	2	Q70V43_CYPCA	Q70v43	cyprinus	ca
25	207.5	44.8	98	2	Q4RQF0_TETNG	Q4rqf0	tetraodon	n
26	206.5	44.6	99	2	Q5ZP81_CYPCA	Q5zpz81	cyprinus	ca
27	122	26.3	98	2	Q8QGV8_PAROL	Q8qgv8	paralichthy	
28	122	26.3	109	2	Q90Y59_PAROL	Q90y59	paralichthy	
29	116	25.1	101	1	IL8_FELCA	Q9xsx5	felis	silve
30	113.5	24.5	101	1	IL8_CAVPO	P49113	cavia	porce
31	113	24.4	97	2	Q6LAE6_HUMAN	Q6lae6	homo	sapien
32	113	24.4	99	1	IL8_HUMAN	P10145	h	interleuk
33	113	24.4	99	2	Q6FGF6_HUMAN	Q6fgf6	homo	sapien
34	112.5	24.3	96	1	GROA_MOUSE	P12850	mus	musculu
35	112.5	24.3	107	2	Q5U5W9_MOUSE	Q5u5w9	mus	musculu
36	111.5	24.1	107	2	Q6PUD4_PIG	Q6pud4	sus	scrofa
37	111	24.0	98	1	SCYBA_RAT	P48973	rattus	norv
38	111	24.0	101	1	IL8_CANFA	P41324	canis	famil
39	110.5	23.9	107	2	Q6PUJ1_PIG	Q6puj1	sus	scrofa
40	110	23.8	103	1	IL8_CHICK	P08317	gallus	gall
41	109.5	23.7	42	2	Q75PL0_ORYLA	Q75pl0	oryzias	lat
42	109.5	23.7	91	1	CCL5_SIGHI	Q91zl1	sigmodon	hi
43	109	23.5	98	2	Q6GTC7_RAT	Q6gtc7	rattus	norv
44	108.5	23.4	91	1	CCL5_MACMU	Q8hyq1	macaca	mula
45	107	23.1	101	1	IL8_MACMU	P67813	macaca	mula

#### ALIGNMENTS

##### RESULT 1

Q6ICW0\_HUMAN

ID Q6ICW0\_HUMAN PRELIMINARY; PRT; 89 AA.

AC Q6ICW0;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE CXCL12 protein (Stromal cell-derived factor 1a) (Fragment).

GN Name=CXCL12;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Zhao X., Zhang H., Lee S., Wong K., Zheng B.;

RT "Polymorphism study of cell-derived factor 1 (SDF1) gene and their

RT correlation with HIV infection in a Chinese cohort.";  
RL Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; CR450283; CAG29279.1; -; mRNA.  
DR EMBL; AY874118; AAW82036.1; -; mRNA.  
FT NON\_TER 89 89  
SQ SEQUENCE 89 AA; 10103 MW; 62B44E8D209C3A14 CRC64;

Query Match 100.0%; Score 463; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 6.2e-44;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
|||||  
Db 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
|||||  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

## RESULT 2

Q9H554\_HUMAN

ID Q9H554\_HUMAN PRELIMINARY; PRT; 92 AA.  
AC Q9H554;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Chemokine (C-X-C motif) ligand 12 (Stromal cell-derived factor  
DE 1).  
GN Name=CXCL12; ORFNames=RP11-20J15.4-002;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Bird C.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AL137026; CAC10202.1; -; Genomic\_DNA.  
DR HSSP; P48061; 1SDF.  
DR SMR; Q9H554; 23-88.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0008009; F:chemokine activity; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00436; INTERLEUKIN8.  
DR SMART; SM00199; SCY; 1.  
SQ SEQUENCE 92 AA; 10510 MW; AEF0C402B44E8D20 CRC64;

Query Match 100.0%; Score 463; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 6.4e-44;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

```

|||||
Db      1 MNAKVVVVLVLVTALCLSDGKPVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIV 60
Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
        |||||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

```

# RESULT 3

## SDF1\_HUMAN

```

ID      SDF1_HUMAN      STANDARD;      PRT;      93 AA.
AC      P48061;
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE      growth stimulating factor) (PBSF) (HIRH) [Contains: SDF-1-beta(3-72);
DE      SDF-1-alpha(3-67)].
GN      Name=CXCL12; Synonyms=SDF1;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RA      Spotila L.D.;
RL      Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=96039262; PubMed=7490086;
RA      Shirozu M., Nakano T., Inazawa J., Tashiro K., Tada H., Shinohara T.,
RA      Honjo T.;
RT      "Structure and chromosomal localization of the human stromal cell-
RT      derived factor 1 (SDF1) gene.";
RL      Genomics 28:495-500(1995).
RN      [3]
RP      NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).
RC      TISSUE=Liver;
RA      Begum N.A., Barnard G.F.;
RT      "Nucleotide sequence of HIRH, human intercrine reduced in hepatomas.";
RL      Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
RN      [4]
RP      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA      Rieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA      Bertucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
RT      "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT      FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL      Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
RN      [5]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX      PubMed=15164054; DOI=10.1038/nature02462;
RA      Deloukas P., Earthworm M.E., Grafham D.V., Rubenfield M., French L.,
RA      Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K.,
RA      Hunt S.E., Andrews T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,
RA      Taylor A., Battles J., Bird C.P., Ainscough R., Almeida J.P.,
RA      Ashwell R.I.S., Ambrose K.D., Babbage A.K., Baggeley C.L., Bailey J.,

```

RA Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,  
 RA Brown J.Y., Burford D.C., Burrill W., Burton J., Cahill P., Camire D.,  
 RA Carter N.P., Chapman J.C., Clark S.Y., Clarke G., Clee C.M., Clegg S.,  
 RA Corby N., Coulson A., Dhami P., Dutta I., Dunn M., Faulkner L.,  
 RA Frankish A., Frankland J.A., Garner P., Garnett J., Gribble S.,  
 RA Griffiths C., Grocock R., Gustafson E., Hammond S., Harley J.L.,  
 RA Hart E., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,  
 RA Huckle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,  
 RA Kimberley A.M., Kershaw J.K., Kokkinaki M., Laird G.K., Lawlor S.,  
 RA Lee H.M., Leongamornlert D.A., Laird G., Lloyd C., Lloyd D.M.,  
 RA Loveland J., Lovell J., McLaren S., McLay K.E., McMurray A.,  
 RA Mashreghi-Mohammadi M., Matthews L., Milne S., Nickerson T.,  
 RA Nguyen M., Overton-Larty E., Palmer S.A., Pearce A.V., Peck A.I.,  
 RA Pelan S., Phillimore B., Porter K., Rice C.M., Rogosin A., Ross M.T.,  
 RA Sarafidou T., Sehra H.K., Shownkeen R., Skuce C.D., Smith M.,  
 RA Standring L., Sycamore N., Tester J., Thorpe A., Torcasso W.,  
 RA Tracey A., Tromans A., Tsolas J., Wall M., Walsh J., Wang H.,  
 RA Weinstock K., West A.P., Willey D.L., Whitehead S.L., Wilming L.,  
 RA Wray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,  
 RA Siebert R., Fechtel K., Bentley D., Durbin R., Hubbard T.,  
 RA Doucette-Stamm L., Beck S., Smith D.R., Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 10.";  
 RL Nature 429:375-381(2004).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP IDENTIFICATION OF SDF-1ALPHA(3-67) AND SDF-1BETA(3-72) BY MASS  
 RP SPECTROMETRY, AND N-TERMINAL AND C-TERMINAL PROCESSING.  
 RX PubMed=14525775; DOI=10.1182/blood-2003-08-2857;  
 RA De La Luz Sierra M., Yang F., Narazaki M., Salvucci O., Davis D.,  
 RA Yarchoan R., Zhang H.H., Fales H., Tosato G.;  
 RT "Differential processing of stromal-derived factor-1alpha and beta  
 RT explains functional diversity.";  
 RL Blood 103:2452-2459(2004).  
 RN [8]

RP STRUCTURE BY NMR OF 22-88.  
 RX MEDLINE=98046030; PubMed=9384579; DOI=10.1093/emboj/16.23.6996;  
 RA Crump M.P., Gong J.H., Loetscher P., Rajarathnam K., Amara A.,  
 RA Arenzana-Seisdedos F., Virelizier J.L., Baggiolini M., Sykes B.D.,  
 RA Clark-Lewis I.;  
 RT "Solution structure and basis for functional activity of stromal cell-  
 RT derived factor-1; dissociation of CXCR4 activation from binding and  
 RT inhibition of HIV-1.";  
 RL EMBO J. 16:6996-7007(1997).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.  
 RX MEDLINE=98284037; PubMed=9618518; DOI=10.1073/pnas.95.12.6941;  
 RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Siani M.A.,  
 RA Lolis E.;  
 RT "Crystal structure of chemically synthesized [N33A] stromal cell-  
 RT derived factor 1alpha, a potent ligand for the HIV-1 'fusin'  
 RT coreceptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).  
 CC -!- FUNCTION: Chemoattractant active on T-lymphocytes, monocytes, but  
 CC not neutrophils. SDF-1-beta(3-72) and SDF-1-alpha(3-67) show a  
 CC reduced chemotactic activity. Binding to cell surface  
 CC proteoglycans seems to inhibit formation of SDF-1-alpha(3-67) and  
 CC thus to preserve activity on local sites.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Beta; Synonyms=SDF-1-beta(1-72);  
 CC IsoId=P48061-1; Sequence=Displayed;  
 CC Name=Alpha; Synonyms=SDF-1-alpha(1-68);  
 CC IsoId=P48061-2; Sequence=VSP\_001056;  
 CC -!- PTM: Processed forms SDF-1-beta(3-72) and SDF-1-alpha(3-67) are  
 CC produced after secretion by proteolytic cleavage of isoforms Beta  
 CC and Alpha, respectively. The N-terminal processing is probably  
 CC achieved by DPP4. Isoform Alpha is first cleaved at the C-terminus  
 CC to yield a SDF-1-alpha(1-67) intermediate before being processed  
 CC at the N-terminus. The C-terminal processing of isoform Alpha is  
 CC reduced by binding to heparin and, probably, cell surface  
 CC proteoglycans.  
 CC -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)  
 CC family.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; U16752; AAA97434.1; -; mRNA.  
 DR EMBL; L36033; AAB39332.1; -; mRNA.  
 DR EMBL; L36034; AAB39333.1; -; mRNA.  
 DR EMBL; U19495; AAB40516.1; -; mRNA.  
 DR EMBL; AY802782; AAV49999.1; -; Genomic\_DNA.  
 DR EMBL; AL137026; CAC10203.1; -; Genomic\_DNA.  
 DR EMBL; BC039893; AAH39893.1; -; mRNA.  
 DR PIR; G01540; G01540.  
 DR PDB; 1A15; X-ray; A/B=22-88.  
 DR PDB; 1QG7; X-ray; A/B=22-88.



DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Stromal cell-derived factor 1 gamma.  
 GN Name=CXCL12;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Callebaut C., Verdin E.;  
 RT "Inhibition of X4 and R5 HIV-1 by human SDF-1g, a novel chemokine that  
 RT interferes with HIV transcription."  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY644456; AAT76437.1; -; mRNA.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0008009; F:chemokine activity; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR PRINTS; PR00436; INTERLEUKIN8.  
 DR SMART; SM00199; SCY; 1.  
 SQ SEQUENCE 119 AA; 13705 MW; C36297D68341B824 CRC64;

Query Match 100.0%; Score 463; DB 2; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-44;  
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
  
 Qy 61 ARLKNNNRQVCIDPKLKWIEYLEKALNK 89  
 ||||||||||||||||||||||||||||  
 Db 61 ARLKNNNRQVCIDPKLKWIEYLEKALNK 89

# RESULT 5

## Q8HYPO\_MACMU

ID Q8HYPO\_MACMU PRELIMINARY; PRT; 89 AA.  
 AC Q8HYPO;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Chemokine CXCL12/SDF-1ALPHA.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecidae; Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;  
 RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;

RT "Molecular cloning and sequencing of 25 different rhesus macaque  
 RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,  
 RT and CX3C families of chemokines.";  
 RL Cytokine 18:140-148(2002).  
 DR EMBL; AF449283; AAN76086.1; -; mRNA.  
 DR HSSP; P48061; 1SDF.  
 DR SMR; Q8HYP0; 23-88.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0008009; F:chemokine activity; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR PRINTS; PR00436; INTERLEUKIN8.  
 DR SMART; SM00199; SCY; 1.  
 SQ SEQUENCE 89 AA; 10105 MW; AD531633C6DC2B07 CRC64;

Query Match 98.3%; Score 455; DB 2; Length 89;  
 Best Local Similarity 97.8%; Pred. No. 4.9e-43;  
 Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
 ||||| |||| |||||  
 Db 1 MNAKVVVVLALVLTTLCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
 Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
 |||||  
 Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

# RESULT 6

## Q5R8M6\_PONPY

ID Q5R8M6\_PONPY PRELIMINARY; PRT; 93 AA.  
 AC Q5R8M6;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Hypothetical protein DKFZp469G1525.  
 GN Name=DKFZp469G1525;  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Pongo.  
 OX NCBI\_TaxID=9600;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Kidney;  
 RG The German cDNA Consortium;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; CR859725; CAH91884.1; -; mRNA.  
 DR SMR; Q5R8M6; 23-88.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0008009; F:chemokine activity; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR002473; C-X-C/Interlkn\_8.





Db

|||||  
61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 8

SDF1\_FELCA

ID SDF1\_FELCA STANDARD; PRT; 93 AA.  
AC O62657;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).  
GN Name=CXCL12; Synonyms=SDF1;  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;  
OC Felinae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (ISOFORMS ALPHA AND BETA).  
RC TISSUE=Thymus;  
RX MEDLINE=98450506; PubMed=9777331;  
RX DOI=10.1046/j.1365-2370.1998.00107.x;  
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,  
RA Cai J.S., Sato E., Kohmoto M., Mikami T.;  
RT "Molecular cloning and sequencing of feline stromal cell-derived  
RT factor-1 alpha and beta."  
RL Eur. J. Immunogenet. 25:303-305(1998).  
CC -!- FUNCTION: Chemoattractant active on T-lymphocytes, monocytes, but  
CC not neutrophils.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Beta;  
CC IsoId=O62657-1; Sequence=Displayed;  
CC Name=Alpha;  
CC IsoId=O62657-2; Sequence=VSP\_001055;  
CC -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)  
CC family.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; AB011966; BAA28602.1; -; mRNA.  
DR HSSP; P48061; 1SDF.  
DR SMR; O62657; 23-88.  
DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR InterPro; IPR001089; CXC\_chmkine\_small.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00436; INTERLEUKIN8.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00471; SMALL\_CYTOKINES\_CXC; FALSE\_NEG.  
KW Alternative splicing; Chemotaxis; Cytokine; Growth factor;



RT "Molecular cloning of TPAR1, a gene whose expression is repressed by  
 RT the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";  
 RL Exp. Cell Res. 215:284-293(1994).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AKR/J;  
 RA Nomura M., Nakata Y., Uzawa A., Nose M., Akashi M., Suzuki G.;  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).  
 RC STRAIN=C57BL/6J; TISSUE=Kidney;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).  
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Chemoattractant active on T-lymphocytes, monocytes, but  
 CC not neutrophils.  
 CC -!- FUNCTION: Stimulates the proliferation of bone marrow-derived b  
 CC progenitor cells in the presence of IL-7 as well as growth of the  
 CC stromal cell-dependent B-cell clone DW34 cells.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Alpha;  
 CC IsoId=P40224-1; Sequence=Displayed;  
 CC Name=Beta;  
 CC IsoId=P40224-2; Sequence=VSP\_001057;  
 CC -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)  
 CC family.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; D21072; BAA04648.1; -; mRNA.  
 DR EMBL; L12029; AAA40100.1; -; mRNA.  
 DR EMBL; L12030; AAA40101.1; -; mRNA.  
 DR EMBL; S74318; AAB32650.1; -; mRNA.  
 DR EMBL; D43804; BAA07862.1; -; mRNA.  
 DR EMBL; D43805; BAA07863.1; -; mRNA.  
 DR EMBL; AK075596; BAC35845.1; -; mRNA.  
 DR EMBL; BC006640; AAH06640.1; -; mRNA.  
 DR PIR; A53497; A53497.  
 DR PIR; I81182; I81182.  
 DR HSSP; P48061; 1SDF.  
 DR SMR; P40224; 23-88.  
 DR Ensembl; ENSMUSG000000061353; Mus musculus.  
 DR MGI; MGI:103556; Cxcl12.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0008009; F:chemokine activity; IDA.  
 DR GO; GO:0007420; P:brain development; IDA.  
 DR GO; GO:0007281; P:germ cell development; IDA.  
 DR GO; GO:0008354; P:germ cell migration; IDA.  
 DR GO; GO:0050930; P:induction of positive chemotaxis; IDA.  
 DR GO; GO:0030335; P:positive regulation of cell migration; IDA.  
 DR GO; GO:0042098; P:T cell proliferation; IMP.  
 DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR InterPro; IPR001089; CXC\_chmkin\_sml1.  
 DR Pfam; PF00048; IL8; 1.  
 DR PRINTS; PR00436; INTERLEUKIN8.  
 DR PROSITE; PS00471; SMALL\_CYTOKINES\_CXC; FALSE\_NEG.

KW Alternative splicing; Chemotaxis; Cytokine; Growth factor;  
 KW Sensory transduction; Signal.  
 FT SIGNAL 1 21 Potential.  
 FT CHAIN 22 89 Stromal cell-derived factor 1.  
 FT DISULFID 30 55 By similarity.  
 FT DISULFID 32 71 By similarity.  
 FT VARSPLIC 89 89 K -> KRLKM (in isoform Beta).  
 FT /FTId=VSP\_001057.  
 SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E55FA CRC64;

Query Match 95.5%; Score 442; DB 1; Length 89;  
 Best Local Similarity 93.3%; Pred. No. 1.4e-41;  
 Matches 83; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCP RFFESHVARANVKHLKILNTPNCALQIV 60  
 |:|||| || ||| |||:|||||||:|||||||  
 Db 1 MDAKVVAVLALVLAALCISDGKPVSLSYRCP RFFESHIARANVKHLKILNTPNCALQIV 60  
 Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
 |||||  
 Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

# RESULT 10

Q543V6\_MOUSE

ID Q543V6\_MOUSE PRELIMINARY; PRT; 89 AA.  
 AC Q543V6;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE 9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched  
 DE library, clone:B130032A21 product:stromal cell derived factor 1, full  
 DE insert sequence.  
 GN Name=Cxcl12;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning."  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes."  
RL Genome Res. 10:1617-1630(2000).

RN [5]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AK045092; BAC32216.1; -; mRNA.  
DR MGI; MGI:103556; Cxcl12.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0008009; F:chemokine activity; IDA.  
DR GO; GO:0007420; P:brain development; IDA.  
DR GO; GO:0007281; P:germ cell development; IDA.  
DR GO; GO:0008354; P:germ cell migration; IDA.  
DR GO; GO:0050930; P:induction of positive chemotaxis; IDA.  
DR GO; GO:0030335; P:positive regulation of cell migration; IDA.  
DR GO; GO:0042098; P:T cell proliferation; IMP.  
SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E55FA CRC64;

Query Match 95.5%; Score 442; DB 2; Length 89;  
Best Local Similarity 93.3%; Pred. No. 1.4e-41;  
Matches 83; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIV 60  
|:|||| || ||| |||:|||||||:|||||||  
Db 1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFESHIRANVKHLKILNTPNCALQIV 60  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
|||||||  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 11  
Q4FJL5\_MOUSE  
ID Q4FJL5\_MOUSE PRELIMINARY; PRT; 93 AA.  
AC Q4FJL5;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)



DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Cxcl12 protein.  
 GN Name=Cxcl12;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,  
 RA Mollenhauer J., Wiemann S., Schick M., Korn B.;  
 RT "Cloning of mouse full open reading frames in Gateway(R) system entry  
 RT vector (pDONR201).";  
 RL Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; CT010389; CAJ18596.1; -; mRNA.  
 SQ SEQUENCE 93 AA; 10561 MW; 625367D344B8AD69 CRC64;

Query Match 95.5%; Score 442; DB 2; Length 93;  
 Best Local Similarity 93.3%; Pred. No. 1.5e-41;  
 Matches 83; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
 |:|||| || ||| |||:|||||||||||||||||||:|||||||||||||||||||  
 Db 1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHIARANVKHLKILNTPNCALQIV 60  
 Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
 |||||||||||||||||||||  
 Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

# RESULT 12

## Q80ZW4\_MOUSE

ID Q80ZW4\_MOUSE PRELIMINARY; PRT; 137 AA.  
 AC Q80ZW4;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cxcl12 protein.  
 GN Name=Cxcl12;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC046827; AAH46827.1; -; mRNA.  
 DR HSSP; P48061; 1SDF.  
 DR SMR; Q80ZW4; 23-88.  
 DR MGI; MGI:103556; Cxcl12.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0008009; F:chemokine activity; IDA.  
 DR GO; GO:0007420; P:brain development; IDA.  
 DR GO; GO:0007281; P:germ cell development; IDA.  
 DR GO; GO:0008354; P:germ cell migration; IDA.  
 DR GO; GO:0050930; P:induction of positive chemotaxis; IDA.  
 DR GO; GO:0030335; P:positive regulation of cell migration; IDA.  
 DR GO; GO:0042098; P:T-cell proliferation; IMP.  
 DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR PRINTS; PR00436; INTERLEUKIN8.  
 DR SMART; SM00199; SCY; 1.  
 SQ SEQUENCE 137 AA; 15529 MW; 04B47DAB6904DF77 CRC64;

Query Match 95.5%; Score 442; DB 2; Length 137;  
 Best Local Similarity 93.3%; Pred. No. 2.1e-41;  
 Matches 83; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVTALCLSDGKPVSLSYRCP RFFESHVARANVKHLKILNTPNCALQIV 60  
 |:|||| || ||| |||:|||||||:|||||||  
 Db 1 MDAKVVAVLALVLAALCISDGKPVSLSYRCP RFFESHIARANVKHLKILNTPNCALQIV 60  
 Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
 |||||  
 Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

# RESULT 13

Q5XNN9\_CANFA

ID Q5XNN9\_CANFA PRELIMINARY; PRT; 89 AA.  
 AC Q5XNN9;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Stromal cell-derived factor-1.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 OC Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Wei Y., Hu S.;  
 RT "Identification and cloning of dog SDF-1 cDNA."  
 RL Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY746395; AAU89475.2; -; mRNA.  
 DR SMR; Q5XNN9; 23-88.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0008009; F:chemokine activity; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR PRINTS; PR00436; INTERLEUKIN8.  
 DR SMART; SM00199; SCY; 1.  
 SQ SEQUENCE 89 AA; 10005 MW; E9B8AD69078E4020 CRC64;

Query Match 94.4%; Score 437; DB 2; Length 89;  
 Best Local Similarity 92.1%; Pred. No. 5.1e-41;  
 Matches 82; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVTALCLSDGKPVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIV 60  
 |:|||| || ||| |||:|||||||:|||||||  
 Db 1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFESHIANANVKHLKILNTPNCALQIV 60  
 Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
 |||||:|||||||  
 Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

#### RESULT 14

##### Q9QZD1\_RAT

ID Q9QZD1\_RAT PRELIMINARY; PRT; 89 AA.  
 AC Q9QZD1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Stromal cell-derived factor-1 alpha (Chemokine (C-X-C motif) ligand  
 DE 12).  
 GN Name=Cxcl12; Synonyms=SDF-1;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Sprague-Dawley;  
 RA Ohtani Y., Okada M., Kawaguchi N., Minami M., Satoh M.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [2]

RP NUCLEOTIDE SEQUENCE.  
RA Pillarisetti K., Gupta S.K.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Kidney;  
RA Director MGC Project;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF189724; AAF01066.1; -; mRNA.  
DR EMBL; AF209976; AAG43506.1; -; mRNA.  
DR EMBL; BC078737; AAH78737.1; -; mRNA.  
DR HSSP; P48061; 1SDF.  
DR SMR; Q9QZD1; 23-88.  
DR Ensembl; ENSRNOG00000013589; Rattus norvegicus.  
DR RGD; 3651; Cxcl12.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0008009; F:chemokine activity; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR002473; C-X-C/Interlkn\_8.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00436; INTERLEUKIN8.  
DR SMART; SM00199; SCY; 1.  
SQ SEQUENCE 89 AA; 9977 MW; D86977626A2E35FA CRC64;

Query Match 94.0%; Score 435; DB 2; Length 89;  
Best Local Similarity 92.1%; Pred. No. 8.6e-41;  
Matches 82; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
|:|||| || ||| |||:||||||||||||||||||||||||||||||||||  
Db 1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

QY 61 ARLKNNRQVCIDPKLKWIQEYLEKALNK 89  
|||:|||||:|||||

Db 61 ARLKSNRROVCIDPKLKWIOEYLDKALNK 89

RESULT 15

Q80YV8 RAT

ID Q80YV8 RAT PRELIMINARY; PRT; 119 AA.

AC 080YV8;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Stromal cell-derived factor-1 gamma.

OS     *Rattus norvegicus* (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Rattus.

OX NCBI TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Gleichmann M., Gillen C., Mueller H.W.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF217564; AAF63712.1; -; mRNA.

DR HSSP; P48061; 1SDF.

DR SMR; Q80YV8; 23-88.

DR GO; GO:0005576; C:extracellular region; IEA.

DR GO; GO:0008009; F:chemokine activity; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR002473; C-X-C/Interlkn 8.

DR InterPro; IPR001811; Chemokine IL8.

DR Pfam; PF00048; IL8; 1.

DR PRINTS; PR00436; INTERLEUKIN8.

DR SMART; SM00199; SCY; 1.

SQ SEQUENCE 119 AA; 13551 MW; 5E1D99E44DC36FA8 CRC64;

Query Match 94.0%; Score 435; DB 2; Length 119;

Best Local Similarity 92.1%; Pred. No. 1.1e-40;

Matches 82; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy            1 MNAKVVVVLVLVTALCLSDGKPVLSYRCPCRFFESHVARANVKHLKIINTPNCALQIV 60  
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Db 1 MDAKVAVLALVLAALCISDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALOIV 60

Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
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Db 61 ARLKSNNRQVCIDPKLKWIQEYLDKALNK 89

Search completed: April 26, 2006, 02:37:30

Job time : 228 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:39:19 ; Search time 25 Seconds  
(without alignments)  
156.650 Million cell updates/sec

Title: US-10-785-230-5  
Perfect score: 463  
Sequence: 1 MNAKVVVVLVLVTALCLSD.....VCIDPKLKWIQEYLEKALNK 89

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
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2: /SIDS5/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /SIDS5/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /SIDS5/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
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6: /SIDS5/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /SIDS5/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /SIDS5/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	463	100.0	89	6	US-10-241-375-22	Sequence 22, Appl
2	463	100.0	89	7	US-11-028-922A-6	Sequence 6, Appli
3	463	100.0	93	6	US-10-241-375-56	Sequence 56, Appl
4	435	94.0	89	7	US-11-028-922A-7	Sequence 7, Appli
5	365	78.8	72	7	US-11-136-097-7	Sequence 7, Appli
6	360	77.8	67	7	US-11-136-097-6	Sequence 6, Appli
7	359	77.5	68	7	US-11-028-922A-5	Sequence 5, Appli
8	351	75.8	67	6	US-10-945-674A-1	Sequence 1, Appli
9	347	74.9	67	6	US-10-945-674A-7	Sequence 7, Appli

10	346	74.7	67	6	US-10-945-674A-3	Sequence 3, Appli
11	346	74.7	67	6	US-10-945-674A-6	Sequence 6, Appli
12	345	74.5	67	6	US-10-945-674A-9	Sequence 9, Appli
13	344	74.3	67	6	US-10-945-674A-2	Sequence 2, Appli
14	344	74.3	67	6	US-10-945-674A-5	Sequence 5, Appli
15	343	74.1	67	6	US-10-945-674A-8	Sequence 8, Appli
16	343	74.1	67	6	US-10-945-674A-133	Sequence 133, App
17	342	73.9	67	6	US-10-945-674A-10	Sequence 10, Appl
18	341	73.7	67	6	US-10-945-674A-4	Sequence 4, Appli
19	339	73.2	67	6	US-10-945-674A-11	Sequence 11, Appl
20	337	72.8	67	6	US-10-945-674A-12	Sequence 12, Appl
21	127.5	27.5	34	6	US-10-945-674A-75	Sequence 75, Appl
22	127.5	27.5	34	6	US-10-945-674A-124	Sequence 124, App
23	127.5	27.5	34	6	US-10-945-674A-126	Sequence 126, App
24	123.5	26.7	34	6	US-10-945-674A-100	Sequence 100, App
25	122.5	26.5	34	6	US-10-945-674A-84	Sequence 84, Appl
26	122.5	26.5	34	6	US-10-945-674A-99	Sequence 99, Appl
27	121.5	26.2	34	6	US-10-945-674A-102	Sequence 102, App
28	120.5	26.0	34	6	US-10-945-674A-83	Sequence 83, Appl
29	120.5	26.0	34	6	US-10-945-674A-86	Sequence 86, Appl
30	119.5	25.8	34	6	US-10-945-674A-101	Sequence 101, App
31	118.5	25.6	34	6	US-10-945-674A-114	Sequence 114, App
32	117.5	25.4	34	6	US-10-945-674A-85	Sequence 85, Appl
33	115.5	24.9	34	6	US-10-945-674A-115	Sequence 115, App
34	113.5	24.5	34	6	US-10-945-674A-116	Sequence 116, App
35	113	24.4	99	6	US-10-241-375-23	Sequence 23, Appl
36	113	24.4	99	7	US-11-186-284-87	Sequence 87, Appl
37	108	23.3	31	6	US-10-945-674A-74	Sequence 74, Appl
38	108	23.3	31	6	US-10-945-674A-123	Sequence 123, App
39	108	23.3	31	6	US-10-945-674A-125	Sequence 125, App
40	106.5	23.0	91	6	US-10-241-375-21	Sequence 21, Appl
41	106.5	23.0	91	7	US-11-262-284-21	Sequence 21, Appl
42	104	22.5	31	6	US-10-945-674A-96	Sequence 96, Appl
43	103	22.2	31	6	US-10-945-674A-80	Sequence 80, Appl
44	103	22.2	31	6	US-10-945-674A-95	Sequence 95, Appl
45	102	22.0	31	6	US-10-945-674A-98	Sequence 98, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-241-375-22

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; Sequence 22, Application US/10241375
; Publication No. US20060073114A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
; APPLICANT: Kanaly, Suzanne T.
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.027US1
; CURRENT APPLICATION NUMBER: US/10/241,375
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US/09/150,813
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: US 08/927939
```

; PRIOR FILING DATE: 1997-09-11  
; NUMBER OF SEQ ID NOS: 105  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 22  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-241-375-22

Query Match 100.0%; Score 463; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.9e-49;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
|  
Db 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
|  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 2

US-11-028-922A-6

; Sequence 6, Application US/11028922A  
; Publication No. US20050271639A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Marc  
; TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS  
; FILE REFERENCE: CCF-7019  
; CURRENT APPLICATION NUMBER: US/11/028,922A  
; CURRENT FILING DATE: 2005-01-04  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-028-922A-6

Query Match 100.0%; Score 463; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 4.9e-49;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
|  
Db 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
|  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 3

US-10-241-375-56

; Sequence 56, Application US/10241375  
; Publication No. US20060073114A1



```
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
; APPLICANT: Kanaly, Suzanne T.
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.027US1
; CURRENT APPLICATION NUMBER: US/10/241,375
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US/09/150,813
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: US 08/927939
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-241-375-56
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Query Match          100.0%; Score 463; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 5.2e-49;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
        ||||||||||||||||||||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

#### RESULT 4

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US-11-028-922A-7
; Sequence 7, Application US/11028922A
; Publication No. US20050271639A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Marc
; TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
; FILE REFERENCE: CCF-7019
; CURRENT APPLICATION NUMBER: US/11/028,922A
; CURRENT FILING DATE: 2005-01-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-028-922A-7
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```
Query Match          94.0%; Score 435; DB 7; Length 89;
Best Local Similarity 92.1%; Pred. No. 1.2e-45;
Matches 82; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
```

```

          |:|||| || ||| |||:|||||||||||||||||||||||||||||||||
Db          1 MDAKVAVLALVLAALCISDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy          61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
          ||||:|||||||||||||||||:|||||
Db          61 ARLKSNNRQVCIDPKLKWIQEYLDKALNK 89

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RESULT 5

US-11-136-097-7

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; Sequence 7, Application US/11136097
; Publication No. US20050265969A1
; GENERAL INFORMATION:
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Gong, Jiang-Hong
; APPLICANT: Duronio, Vincent
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080352-000000US
; CURRENT APPLICATION NUMBER: US/11/136,097
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: US/09/646,192
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,226,391
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: stromal cell derived factor-1beta (SDF-1beta)

```

US-11-136-097-7

```

Query Match          78.8%; Score 365; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy          22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
          |||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy          82 YLEKALNK 89
          |||||||
Db          61 YLEKALNK 68

```

RESULT 6

US-11-136-097-6

```

; Sequence 6, Application US/11136097
; Publication No. US20050265969A1
; GENERAL INFORMATION:

```

```
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Gong, Jiang-Hong
; APPLICANT: Duronio, Vincent
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
; FILE REFERENCE: 080352-000000US
; CURRENT APPLICATION NUMBER: US/11/136,097
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: US/09/646,192
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: CA 2,226,391
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: CA 2,245,224
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: stromal cell derived factor-1alpha (SDF-1alpha)
US-11-136-097-6
```

```
Query Match          77.8%; Score 360; DB 7; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.1e-36;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy      82 YLEKALN 88
          |||||
Db      61 YLEKALN 67
```

# RESULT 7

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US-11-028-922A-5
; Sequence 5, Application US/11028922A
; Publication No. US20050271639A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Marc
; TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
; FILE REFERENCE: CCF-7019
; CURRENT APPLICATION NUMBER: US/11/028,922A
; CURRENT FILING DATE: 2005-01-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-028-922A-5
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Query Match 77.5%; Score 359; DB 7; Length 68;  
Best Local Similarity 98.5%; Pred. No. 1.5e-36;  
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       1 KPVSLLYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy      82 YLEKALNK 89
          |||||
Db      61 YLEKALNK 68
```

RESULT 8

US-10-945-674A-1

; Sequence 1, Application US/10945674A  
; Publication No. US20060014682A1  
; GENERAL INFORMATION:  
; APPLICANT: Tudan, Christopher R.  
; APPLICANT: Merzouk, Ahmed  
; APPLICANT: Arab, Lakhdar  
; APPLICANT: Saxena, Geeta  
; APPLICANT: Eaves, Connie J.  
; APPLICANT: Cashman, Joanne  
; APPLICANT: Clark-Lewis, Ian  
; APPLICANT: Salari, Hassan  
; APPLICANT: Chemokine Therapeutics Corporation  
; APPLICANT: The University of British Columbia  
; TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells  
; FILE REFERENCE: 080420-000100US  
; CURRENT APPLICATION NUMBER: US/10/945,674A  
; CURRENT FILING DATE: 2004-09-20  
; PRIOR APPLICATION NUMBER: CA 2,305,787  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: US 60/205,467  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 09/852,424  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic  
; OTHER INFORMATION: SDF-1(1-67)[P2G] CXCR4 receptor antagonist  
US-10-945-674A-1

Query Match 75.8%; Score 351; DB 6; Length 67;  
Best Local Similarity 98.5%; Pred. No. 1.3e-35;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       1 KGVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60
```

Qy 82 YLEKALN 88  
| | | | |  
Db 61 YLEKALN 67

RESULT 9

US-10-945-674A-7

; Sequence 7, Application US/10945674A  
; Publication No. US20060014682A1  
; GENERAL INFORMATION:  
; APPLICANT: Tudan, Christopher R.  
; APPLICANT: Merzouk, Ahmed  
; APPLICANT: Arab, Lakhdar  
; APPLICANT: Saxena, Geeta  
; APPLICANT: Eaves, Connie J.  
; APPLICANT: Cashman, Joanne  
; APPLICANT: Clark-Lewis, Ian  
; APPLICANT: Salari, Hassan  
; APPLICANT: Chemokine Therapeutics Corporation  
; APPLICANT: The University of British Columbia  
; TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells  
; FILE REFERENCE: 080420-000100US  
; CURRENT APPLICATION NUMBER: US/10/945,674A  
; CURRENT FILING DATE: 2004-09-20  
; PRIOR APPLICATION NUMBER: CA 2,305,787  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: US 60/205,467  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 09/852,424  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic  
; OTHER INFORMATION: SDF-1[P2G] CXCR4 receptor antagonist analogue  
; OTHER INFORMATION: with proline-amino acid chimera (P\*) substituted  
; OTHER INFORMATION: at residue 6  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (6)  
; OTHER INFORMATION: Xaa = P\* = proline-amino acid chimera (3-aryl-proline,  
; OTHER INFORMATION: 3-hydroxyaryl-proline or 3-alkyl-proline)  
US-10-945-674A-7

Query Match 74.9%; Score 347; DB 6; Length 67;  
Best Local Similarity 97.0%; Pred. No. 4.1e-35;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81  
| | | | |  
Db 1 KGVSLXYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60  
  
Qy 82 YLEKALN 88

|||||

US-10-945-674A-3

US-10-945-674A-3

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 82 YLEKALN 88

US-10-945-674A-6

; Sequence 6, Application US/10945674A



```
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Joanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; APPLICANT: Chemokine Therapeutics Corporation
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells
; FILE REFERENCE: 080420-000100US
; CURRENT APPLICATION NUMBER: US/10/945,674A
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/852,424
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: SDF-1[P2G] CXCR4 receptor antagonist analogue
; OTHER INFORMATION: with proline-amino acid chimera (P*) substituted
; OTHER INFORMATION: at residue 8
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: Xaa = P* = proline-amino acid chimera (3-aryl-proline,
; OTHER INFORMATION: 3-hydroxyaryl-proline or 3-alkyl-proline)
US-10-945-674A-9
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Query Match          74.5%; Score 345; DB 6; Length 67;
Best Local Similarity 97.0%; Pred. No. 7.1e-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
|       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  KGVSLSYXCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy      82 YLEKALN 88
|       | | | | | |
Db      61 YLEKALN 67
```

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RESULT 13
US-10-945-674A-2
; Sequence 2, Application US/10945674A
; Publication No. US20060014682A1
; GENERAL INFORMATION:
```



```
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Joanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; APPLICANT: Chemokine Therapeutics Corporation
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells
; FILE REFERENCE: 080420-000100US
; CURRENT APPLICATION NUMBER: US/10/945,674A
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/852,424
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: SDF-1(1-67)[P2G] CXCR4 receptor antagonist
; OTHER INFORMATION: analogue with proline (P) substituted at residue 5
US-10-945-674A-2
```

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Query Match          74.3%; Score 344; DB 6; Length 67;
Best Local Similarity 97.0%; Pred. No. 9.4e-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  KGVSPSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy      82 YLEKALN 88
          | | | | |
Db      61 YLEKALN 67
```

#### RESULT 14

US-10-945-674A-5

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; Sequence 5, Application US/10945674A
; Publication No. US20060014682A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Joanne
; APPLICANT: Clark-Lewis, Ian
```





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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:38:29 ; Search time 165 Seconds  
(without alignments)  
225.375 Million cell updates/sec

Title: US-10-785-230-5  
Perfect score: 463  
Sequence: 1 MNAKVVVVLVLVLTALCLSD.....VCIDPKLKWIQEYLEKALNK 89

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	463	100.0	89	2	US-08-927-939-22	Sequence 22, Appl
2	463	100.0	89	3	US-09-953-692-4	Sequence 4, Appli
3	463	100.0	89	3	US-09-953-717-4	Sequence 4, Appli
4	463	100.0	89	3	US-09-792-793A-32	Sequence 32, Appl
5	463	100.0	89	4	US-10-375-209A-32	Sequence 32, Appl
6	463	100.0	89	4	US-10-785-230-5	Sequence 5, Appli
7	463	100.0	89	5	US-10-924-029-1	Sequence 1, Appli
8	463	100.0	89	5	US-10-985-324-4	Sequence 4, Appli
9	463	100.0	89	5	US-10-773-236-280	Sequence 280, App
10	463	100.0	89	5	US-10-921-235-43	Sequence 43, Appl
11	463	100.0	93	2	US-08-927-939-56	Sequence 56, Appl

12	463	100.0	93	3	US-09-144-838-7	Sequence 7, Appli
13	463	100.0	93	3	US-09-919-497-95	Sequence 95, Appl
14	463	100.0	93	3	US-09-835-107-2	Sequence 2, Appli
15	463	100.0	93	3	US-09-835-107-3	Sequence 3, Appli
16	463	100.0	93	3	US-09-792-793A-93	Sequence 93, Appl
17	463	100.0	93	4	US-10-086-177A-2	Sequence 2, Appli
18	463	100.0	93	4	US-10-086-177A-3	Sequence 3, Appli
19	463	100.0	93	4	US-10-375-209A-93	Sequence 93, Appl
20	463	100.0	93	4	US-10-447-315-25	Sequence 25, Appl
21	463	100.0	93	4	US-10-706-265-6	Sequence 6, Appli
22	463	100.0	93	4	US-10-788-792-193	Sequence 193, App
23	463	100.0	93	5	US-10-723-860-2672	Sequence 2672, Ap
24	463	100.0	93	5	US-10-924-029-2	Sequence 2, Appli
25	463	100.0	93	5	US-10-222-703A-3	Sequence 3, Appli
26	463	100.0	93	5	US-10-222-703A-4	Sequence 4, Appli
27	463	100.0	93	5	US-10-849-989-28	Sequence 28, Appl
28	463	100.0	93	5	US-10-756-149-5439	Sequence 5439, Ap
29	463	100.0	93	5	US-10-287-436A-522	Sequence 522, App
30	463	100.0	93	5	US-10-287-436A-1213	Sequence 1213, Ap
31	463	100.0	119	4	US-10-308-322-12	Sequence 12, Appl
32	463	100.0	166	4	US-10-335-394-5	Sequence 5, Appli
33	442	95.5	89	4	US-10-785-230-7	Sequence 7, Appli
34	435	94.0	93	4	US-10-308-322-17	Sequence 17, Appl
35	435	94.0	119	4	US-10-308-322-13	Sequence 13, Appl
36	428	92.4	136	4	US-10-264-049-3373	Sequence 3373, Ap
37	427	92.2	90	4	US-10-308-322-7	Sequence 7, Appli
38	427	92.2	119	4	US-10-308-322-4	Sequence 4, Appli
39	377	81.4	74	4	US-10-050-902-238	Sequence 238, App
40	377	81.4	74	4	US-10-050-898-238	Sequence 238, App
41	377	81.4	101	4	US-10-308-322-22	Sequence 22, Appl
42	377	81.4	177	4	US-10-335-394-54	Sequence 54, Appl
43	377	81.4	339	4	US-10-335-394-55	Sequence 55, Appl
44	376	81.2	70	4	US-10-050-902-239	Sequence 239, App
45	376	81.2	70	4	US-10-050-898-239	Sequence 239, App

#### ALIGNMENTS

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RESULT 1
US-08-927-939-22
; Sequence 22, Application US/08927939
; Publication No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-08-927-939-22

Query Match 100.0%; Score 463; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.2e-47;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCPCRRFFESHVARANVKHLKILNTPNCALQIV 60  
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Db 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCPCRRFFESHVARANVKHLKILNTPNCALQIV 60  
  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
|  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 2

US-09-953-692-4

; Sequence 4, Application US/09953692  
; Patent No. US20020107195A1  
; GENERAL INFORMATION:  
; APPLICANT: Shalley, Gupta K.  
; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by  
; TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1(  
; FILE REFERENCE: P50676C1  
; CURRENT APPLICATION NUMBER: US/09/953,692  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: 09/358,624  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: 60/093,596  
; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Human  
US-09-953-692-4

Query Match 100.0%; Score 463; DB 3; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.2e-47;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCPCRRFFESHVARANVKHLKILNTPNCALQIV 60  
  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
|  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 3

US-09-953-717-4

; Sequence 4, Application US/09953717  
; Patent No. US20020107196A1  
; GENERAL INFORMATION:  
; APPLICANT: Shalley, Gupta K.



US-09-792-793A-32

Query Match 100.0%; Score 463; DB 3; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.2e-47;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
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Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 5

US-10-375-209A-32

; Sequence 32, Application US/10375209A  
; Publication No. US20030215421A1  
; GENERAL INFORMATION:  
; APPLICANT: McDonald, John R.  
; APPLICANT: Coggins, Philip  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE  
DAMAGE AND  
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
; FILE REFERENCE: 25020-601E  
; CURRENT APPLICATION NUMBER: US/10/375,209A  
; CURRENT FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human Chemokine Polypeptide: Stromal cell-derived  
; OTHER INFORMATION: Factor-1-Alpha (SDF-1-Alpha)  
; PUBLICATION INFORMATION:  
; JOURNAL: Genomics  
; VOLUME: 28  
; PAGES: 495-500  
; DATE: 1995  
US-10-375-209A-32

Query Match 100.0%; Score 463; DB 4; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.2e-47;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNAKVVVVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
|  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89



# RESULT 6

US-10-785-230-5

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; Sequence 5, Application US/10785230
; Publication No. US20040209837A1
; GENERAL INFORMATION:
; APPLICANT: KISHIMOTO, Tadamitsu
; APPLICANT: NAGASAWA, Takashi
; APPLICANT: TACHIBANA, Kazunobu
; APPLICANT: CHUGAI SEIYAKU KABUSIKI KAISHA
; TITLE OF INVENTION: Vascularization Inhibitors
; FILE REFERENCE: 46124-5042-US
; CURRENT APPLICATION NUMBER: US/10/785,230
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: PCT/JP99/01448
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: JP10/95448
; PRIOR FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ligand peptide
US-10-785-230-5

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Query Match          100.0%; Score 463; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e-47;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

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# RESULT 7

US-10-924-029-1

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; Sequence 1, Application US/10924029
; Publication No. US20050020528A1
; GENERAL INFORMATION:
; APPLICANT: Herrmann, Stephen H.
;           Lu, Zhijian
;           McCoy, John M.
;           Swanberg, Stephen L.
;           Walker, Bruce
;           Yang, Otto
; TITLE OF INVENTION: CHEMOKINES WITH AMINO-TERMINAL MODIFICATIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA

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;          COUNTRY: U.S.A.
;          ZIP: 02140
;    COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/10/924,029
;          FILING DATE: 23-Aug-2004
;          CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/09/175,713
;          FILING DATE: 20-Oct-1998
;    ATTORNEY/AGENT INFORMATION:
;          NAME: Sprunger, Suzanne A.
;          REGISTRATION NUMBER: 41,323
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (617) 498-8284
;          TELEFAX: (617) 876-5851
;    INFORMATION FOR SEQ ID NO: 1:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 89 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-924-029-1

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Query Match          100.0%;  Score 463;  DB 5;  Length 89;
Best Local Similarity 100.0%;  Pred. No. 1.2e-47;
Matches 89;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

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RESULT 8
US-10-985-324-4
; Sequence 4, Application US/10985324
; Publication No. US20050202019A1
; GENERAL INFORMATION:
; APPLICANT: Northwest Biotherapeutics, Inc.
; APPLICANT: Murphy, Gerald P.
; APPLICANT: Boynton, Alton L.
; APPLICANT: Sehgal, Anil
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED ON THE
; TITLE OF INVENTION: ROLE OF THE CXCR-4 GENE IN TUMORIGENESIS
; FILE REFERENCE: 20093-000600PC
; CURRENT APPLICATION NUMBER: US/10/985,324
; CURRENT FILING DATE: 2004-11-09

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; PRIOR APPLICATION NUMBER: US/09/647,501
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/079,916
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/104,656
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-985-324-4
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Query Match          100.0%; Score 463; DB 5; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e-47;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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# RESULT 9

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US-10-773-236-280
; Sequence 280, Application US/10773236
; Publication No. US20050208602A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al.
; TITLE OF INVENTION: 89 Human Secreted Proteins
; FILE REFERENCE: PS751P1
; CURRENT APPLICATION NUMBER: US/10/773,236
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/311,085
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,209
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: PCT/US02/25107
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/330,629
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US02/33985
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/331,046
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: PCT/US02/35606
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/358,554
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: PCT/US03/04819
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/358,714
; PRIOR FILING DATE: 2002-02-25
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Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 11

US-08-927-939-56

; Sequence 56, Application US/08927939  
; Publication No. US20010006640A1  
; GENERAL INFORMATION:  
; APPLICANT: Grainger, David J.  
; APPLICANT: Tatalick, Lauen Marie  
; TITLE OF INVENTION: Compounds and methods to inhibit or  
; TITLE OF INVENTION: augment an inflammatory response.  
; FILE REFERENCE: 295.022US1  
; CURRENT APPLICATION NUMBER: US/08/927,939  
; CURRENT FILING DATE: 1997-09-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 56  
; LENGTH: 93  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-927-939-56

Query Match 100.0%; Score 463; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1.3e-47;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
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Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 12

US-09-144-838-7

; Sequence 7, Application US/09144838A  
; Patent No. US20020051996A1  
; GENERAL INFORMATION:  
; APPLICANT: Siani, Michael A.  
; APPLICANT: Wilken, Jill  
; APPLICANT: Simon, Reyna  
; APPLICANT: Kent, Stephen B.H.  
; TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation  
; FILE REFERENCE: GREN-020/01US  
; CURRENT APPLICATION NUMBER: US/09/144,838A  
; CURRENT FILING DATE: 1998-08-31  
; EARLIER APPLICATION NUMBER: US 60/057,620  
; EARLIER FILING DATE: 1997-09-04  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 93  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-144-838-7

Query Match 100.0%; Score 463; DB 3; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1.3e-47;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
|  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 13

US-09-919-497-95  
; Sequence 95, Application US/09919497  
; Patent No. US2002010662A1  
; GENERAL INFORMATION:  
; APPLICANT: Mutter, George L.  
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER  
; FILE REFERENCE: B0801/7225  
; CURRENT APPLICATION NUMBER: US/09/919,497  
; CURRENT FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: US 60/221,735  
; PRIOR FILING DATE: 2000-07-31  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 95  
; LENGTH: 93  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-919-497-95

Query Match 100.0%; Score 463; DB 3; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1.3e-47;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
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Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 14

US-09-835-107-2  
; Sequence 2, Application US/09835107  
; Patent No. US20020165123A1  
; GENERAL INFORMATION:  
; APPLICANT: Tudan, Christopher R.

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; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SDF-1 Precursor, PBSF
US-09-835-107-2

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Query Match          100.0%; Score 463; DB 3; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.3e-47;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
        |||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

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# RESULT 15

US-09-835-107-3

```

; Sequence 3, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20

```





GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 26, 2006, 02:30:09 ; Search time 187 Seconds  
(without alignments)  
209.116 Million cell updates/sec

Title: US-10-785-230-5  
Perfect score: 463  
Sequence: 1 MNAKVVVVLVLVTALCLSD.....VCIDPKLKWIQEYLEKALNK 89

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	463	100.0	89	2	AAR75419	Aar75419 Human SDF
2	463	100.0	89	2	AAAY26177	Aay26177 Stromal c
3	463	100.0	89	2	AAAY39995	Aay39995 Human SDF
4	463	100.0	89	3	AAAY52508	Aay52508 Human str
5	463	100.0	89	3	AAAY93603	Aay93603 A human B
6	463	100.0	89	3	AAB15791	Aab15791 Human che
7	463	100.0	89	5	ABG32978	Abg32978 Human str
8	463	100.0	89	5	ABG33066	Abg33066 Human str

9	463	100.0	89	7	ADC78236	Adc78236	Human	sec
10	463	100.0	89	9	ADW64706	Adw64706	Human	che
11	463	100.0	93	2	AAR75420	Aar75420	Human	SDF
12	463	100.0	93	2	AAW50766	Aaw50766	Human	SDF
13	463	100.0	93	2	AAZ26178	Aay26178	Stromal	c
14	463	100.0	93	2	AAZ06725	Aay06725	Amino	aci
15	463	100.0	93	3	AAB15812	Aab15812	Human	che
16	463	100.0	93	5	AAU84305	Aau84305	Human	end
17	463	100.0	93	5	AAB47691	Aab47691	SDF-1	bet
18	463	100.0	93	5	AAB47690	Aab47690	SDF-1	pre
19	463	100.0	93	5	AAE23952	Aae23952	Human	str
20	463	100.0	93	7	ADN95190	Adn95190	Human	BEC
21	463	100.0	93	7	ADP65272	Adp65272	Human	str
22	463	100.0	93	8	ADN07719	Adn07719	Human	str
23	463	100.0	93	8	ADP12445	Adp12445	Protein	e
24	463	100.0	93	8	ADQ19853	Adq19853	Human	sof
25	463	100.0	93	8	ADQ14484	Adq14484	Human	che
26	463	100.0	93	8	ADR99187	Adr99187	Chemokine	
27	463	100.0	93	9	ADW64707	Adw64707	Human	che
28	463	100.0	93	9	ADY76111	Ady76111	Human	str
29	463	100.0	93	9	ADY76110	Ady76110	Human	str
30	463	100.0	93	9	ADZ21672	Adz21672	Human	str
31	463	100.0	119	5	AAM48047	Aam48047	Human	SDF
32	463	100.0	166	2	AAZ29899	Aay29899	Human	SDF
33	463	100.0	328	2	AAW76220	Aaw76220	Human	che
34	454	98.1	93	8	ADN36543	Adn36543	Chemokine	
35	447.5	96.7	92	8	ADN36544	Adn36544	Chemokine	
36	442	95.5	89	2	AAR70994	Aar70994	Protein	e
37	442	95.5	89	2	AAW50764	Aaw50764	Peptide	#
38	442	95.5	89	2	AAZ39996	Aay39996	Mouse	SDF
39	442	95.5	89	6	AAE14828	Aae14828	Mouse	str
40	442	95.5	93	2	AAW50765	Aaw50765	Peptide	#
41	440	95.0	326	2	AAW76221	Aaw76221	Human	che
42	435	94.0	93	5	AAM48049	Aam48049	Rat	SDF-1
43	435	94.0	119	5	AAM48048	Aam48048	Rat	SDF-1
44	428	92.4	136	5	ABP42241	Abp42241	Human	ova
45	427	92.2	90	5	AAM48043	Aam48043	Generic	S

# ALIGNMENTS

## RESULT 1

AAR75419

ID AAR75419 standard; protein; 89 AA.

XX

AC AAR75419;

XX

DT 15-NOV-1995 (first entry)

XX

DE Human SDF-1-alpha.

XX

KW SDF-1-alpha; stromal derived factor; hematopoietic cell;

KW inflammatory disease; infectious disease; AIDS;

KW neurodegenerative disease.

XX

OS Homo sapiens.

XX  
 FH Key Location/Qualifiers  
 FT Peptide 1. .21  
 FT /label= Sig\_peptide  
 XX  
 PN CA2117953-A.  
 XX  
 PD 15-APR-1995.  
 XX  
 PF 12-OCT-1994; 94CA-02117953.  
 XX  
 PR 14-OCT-1993; 93JP-00280505.  
 XX  
 PA (ONOH ) ONO PHARM CO LTD.  
 XX  
 PI Honjo T, Shirozu M, Tada H;  
 XX  
 DR WPI; 1995-207311/28.  
 DR N-PSDB; AAQ74088, AAQ74089.  
 XX  
 PT Polypeptide(s) used for treating diseases relating to undergrown or  
 PT abnormal proliferation of haematopoietic cells - e.g. inflammatory  
 PT diseases, infectious diseases, AIDS or neuro:degenerative diseases.  
 XX  
 PS Claim 2; Page 22; 43pp; English.  
 XX  
 CC A cDNA library prepared from human pro-B cell line FLEB14 cells was  
 CC screened with 32P-labeled mouse SDF-1-alpha cDNA. A positive clone  
 CC contained an insert of 1.9 kb (AAQ74089), including an ORF (AAQ74088)  
 CC encoding human SDF-1-alpha (AAR75419). Recombinant hSDF-1-alpha was  
 CC produced in E. coli and COS cells  
 XX  
 SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 2; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-49;  
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
 |||||  
 Db 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
 Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
 |||||  
 Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 2  
 AAY26177  
 ID AAY26177 standard; protein; 89 AA.  
 XX  
 AC AAY26177;  
 XX  
 DT 29-SEP-1999 (first entry)  
 XX  
 DE Stromal cell derived factor 1a.  
 XX

```

KW      Stromal cell derived factor 1a; SDF1a; vaccine; immune response;
KW      antigen; humoral response; cell-mediated response; PCR;
KW      immunostimulatory; expression plasmid vector.
XX
OS      Homo sapiens.
XX
FH      Key                Location/Qualifiers
FT      Peptide            1. .21
FT                        /note= "signal peptide"
FT      Protein            22. .89
FT                        /label= SDF_1a
FT                        /note= "Stromal cell-derived factor-1a"
XX
PN      WO9929728-A1.
XX
PD      17-JUN-1999.
XX
PF      11-DEC-1998;      98WO-US026291.
XX
PR      11-DEC-1997;      97US-0069281P.
XX
PA      (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI      Gallo RC,  Devico AL,  Garzino-Demo A;
XX
DR      WPI; 1999-385578/32.
DR      N-PSDB; AAX80632.
XX
PT      Methods of enhancing vaccine efficacy.
XX
PS      Claim 4; Page 102; 134pp; English.
XX
CC      The present sequence is stromal cell derived factor-1a. This belongs to
CC      the CXC class of chemokines. This is chemotactic for mature dendritic
CC      cells. The efficacy of a vaccine is enhanced by combining it with one or
CC      more chemokines to enhance the immune response to an antigen. This can be
CC      humoral or cell-mediated immune response. The purified chemokines,
CC      fragments, derivatives or analogues are administered either concurrently
CC      with one or more purified antigens against which an immune response is
CC      desired or within a time period either before or after antigen
CC      administration. The chemokine gene is isolated by PCR, and administered
CC      by constructing an expression plasmid vector which can be expressed in a
CC      coordinated manner upon introduction in a suitable cell. The vaccines are
CC      immunostimulatory and can be used to treat microbial diseases especially
CC      HIV
XX
SQ      Sequence 89 AA;

```

|||||  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 3

AAAY39995

ID AAY39995 standard; protein; 89 AA.

XX

AC AAY39995;

XX

DT 16-DEC-1999 (first entry)

XX

DE Human SDF-1-alpha protein sequence.

XX

KW CXCR4; human; neovascularisation; inhibitor; solid cancer; therapy;

KW tissue repairing agent; vascularisation; SDF-1-alpha.

XX

OS Homo sapiens.

XX

PN WO9948528-A1.

XX

PD 30-SEP-1999.

XX

PF 23-MAR-1999; 99WO-JP001448.

XX

PR 24-MAR-1998; 98JP-00095448.

XX

PA (CHUS ) CHUGAI SEIYAKU KK.

PA (KISH/) KISHIMOTO T.

XX

PI Kishimoto T, Nagasawa T, Tachibana K;

XX

DR WPI; 1999-591042/50.

DR N-PSDB; AAZ27612.

XX

PT CXCR4-potentiating agents and methods useful for inhibiting

PT neovascularization, and treating solid cancers.

XX

PS Disclosure; Page 51-52; 63pp; Japanese.

XX

CC This sequence is the human SDF-1-alpha protein. The invention relates to  
CC remedies inhibiting neovascularisation, remedies for solid cancer,  
CC remedies for diseases pathologically caused by neovascularisation and  
CC tissue repairing agents containing as the active ingredient a substance  
CC capable of potentiating CXCR4. Based on a finding that vascularisation is  
CC inhibited in a CXCR4 knockout mouse, it becomes possible to prepare  
CC remedies inhibiting vascularisation which contain as the active  
CC ingredient a substance capable of potentiating CXCR4, remedies for solid  
CC cancer, remedies for diseases pathologically caused by neovascularisation  
CC and tissue repairing agents containing as the active ingredient a  
CC substance capable of potentiating CXCR4. It is also possible to establish  
CC methods for treatment with the use of these remedies

XX

SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.4e-49;

Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
          |||
Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
          |||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 4

AAAY52508

ID AAY52508 standard; protein; 89 AA.

XX

AC AAY52508;

XX

DT 22-FEB-2000 (first entry)

XX

DE Human stromal cell derived factor-1 (SDF-1).

XX

KW CXC-chemokine receptor-4; CXCR-4; stromal cell derived factor-1; SDF-1;

KW ligand; chemotaxis; inflammation; G-protein-coupled receptor;

KW signal transduction; CD4-independent; HIV-1; infection; proliferation;

KW transformation; tumorigenesis; cancer; tumour; overexpression; brain;

KW breast; colon; lung; melanoma; glioblastoma; inhibition; growth arrest;

KW diagnosis; prognosis; marker; proliferative disorders; antisense;

KW therapy; treatment; premalignant condition; hypertrophy;

KW degenerative disorder; Parkinson's disease; Alzheimer's disease;

KW growth deficiency; hypoproliferative disorder; physical trauma; lesion;

KW ischaemia; wound.

XX

OS Homo sapiens.

XX

PN WO9950461-A1.

XX

PD 07-OCT-1999.

XX

PF 29-MAR-1999; 99WO-US007431.

XX

PR 30-MAR-1998; 98US-0079916P.

PR 16-OCT-1998; 98US-0104656P.

XX

PA (NWBI-) NORTHWEST BIOTHERAPEUTICS INC.

XX

PI Murphy GP, Boynton AL, Sehgal A;

XX

DR WPI; 2000-052634/04.

DR N-PSDB; AAZ38554.

XX

PT Use of CXCR-4 and SDF-1 as markers for diagnosis and treatment of e.g.

PT tumors, degenerative disorders, growth deficiencies, hyper- and

PT hypoproliferative disorders, physical trauma, lesions and wounds.

XX

PS Disclosure; Fig 15; 138pp; English.

XX

CC This sequence represents stromal cell derived factor-1 (SDF-1) cDNA. SDF-

CC 1 is the ligand for CXC-chemokine receptor-4 (CXCR-4, AAY52507).  
 CC Chemokine receptors play an important role in the chemotaxis of T-cells  
 CC and phagocytic cells to areas of inflammation. CXCR-4 is a member of the  
 CC G-protein-coupled receptor family, which is involved in signal  
 CC transduction. CXCR-4 also mediates CD4-independent infection by HIV-1.  
 CC CXCR-4 has now been found to have a role in the aberrant proliferative  
 CC behaviour of a number of cell types, including numerous primary tumours  
 CC and derived cell lines. CXCR-4 is involved in cell transformation and  
 CC tumorigenesis, particularly in brain, breast and colon tumours. It was  
 CC found to be overexpressed in several brain tumour derived cell lines and  
 CC primary brain tumour tissues, breast tumour tissues, colorectal  
 CC adenocarcinoma, lung carcinoma and melanoma cell lines. CXCR-4 expression  
 CC was required for the continuous proliferation of glioblastoma cancer  
 CC cells, and inhibition of its gene function resulted in growth arrest.  
 CC Conversely, overexpression resulted in enhanced and rapid cellular  
 CC proliferation. CXCR-4 and SDF-1 can be used as markers for the diagnosis  
 CC and prognosis of cell proliferative disorders, and antisense  
 CC oligonucleotides complementary to at least a portion of an RNA transcript  
 CC of a CXCR-4 gene can be used to inhibit hyperproliferation of a tumour  
 CC cell. Agents that inhibit CXCR-4 function can be used for treating or  
 CC preventing a disease or disorder involving cell overproliferation, e.g.,  
 CC brain cancer, breast cancer, colon cancer, prostate cancer and B cell  
 CC lymphoma, and also premalignant conditions, benign tumours,  
 CC hyperproliferative disorders, and benign dysproliferative disorders. They  
 CC can also be used for treating e.g., cirrhosis of the liver, keloid  
 CC formation, psoriasis, benign tumors, fibrocystic conditions and tissue  
 CC hypertrophy. Compounds that promote CXCR-4 function can also be used for  
 CC preventing or treating a disease or disorder involving a deficiency in  
 CC cell proliferation, or treating a condition where cell proliferation  
 CC would be desirable. Such diseases include degenerative disorders (e.g.,  
 CC Parkinson's disease, Alzheimer's disease), growth deficiencies,  
 CC hypoproliferative disorders, physical trauma, lesions (e.g., those caused  
 CC by ischaemia), and wounds  
 XX  
 SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 3; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-49;  
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCREFFESHVARANVKHLKILNTPNCALQIV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCREFFESHVARANVKHLKILNTPNCALQIV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
 ||||||||||||||||||||||||||||  
 Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 5  
 AAY93603  
 ID AAY93603 standard; protein; 89 AA.  
 XX  
 AC AAY93603;  
 XX  
 DT 25-SEP-2000 (first entry)  
 XX

DE A human B-cell stimulating factor homologue (SDFla).  
 XX  
 KW Differentially expressed human gene; cardiac disease; kidney disease;  
 KW inflammatory disease; I-8U; prostacyclin-stimulating factor; isf-2;  
 KW tissue specific mRNA; insulin-like growth factor binding protein 6;  
 KW OSF-1; gas-1; YMP; BTG2; pre-B cell stimulating factor homologue; SDFla;  
 KW peripheral benzodiazepine receptor; annexin II cellular ligand; pll;  
 KW congenital heart failure; dilated congestive cardiomyopathy;  
 KW hypertrophic cardiomyopathy; restrictive cardiomyopathy;  
 KW mitral valve disease; aortic valve disease; tricuspid valve disease;  
 KW angina pectoris; myocardial infarction; cardiac arrhythmia;  
 KW pulmonary hypertension; arterial hypertension; renovascular hypertension;  
 KW arteriosclerosis; atherosclerosis; cardiac tumour.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200035473-A2.  
 XX  
 PD 22-JUN-2000.  
 XX  
 PF 15-DEC-1999; 99WO-US029941.  
 XX  
 PR 18-DEC-1998; 98US-0113008P.  
 XX  
 PA (SCIO-) SCIOS INC.  
 XX  
 PI Stanton LW, White RT, Damm DL, Lewicki JA, Joly A, Schreiner GF;  
 XX  
 DR WPI; 2000-451904/39.  
 DR N-PSDB; AAA46677.  
 XX  
 PT Preventing, diagnosing and treating cardiac, kidney and inflammatory  
 PT disorders using cardiac genes that are differentially expressed in  
 PT disease states such as cardiac arrhythmia and arteriosclerosis.  
 XX  
 PS Disclosure; Fig 8J; 170pp; English.  
 XX  
 CC AAY93594-Y93605 are encoded by differentially expressed human genes,  
 CC associated with disease states and disorders. The specification describes  
 CC methods preventing, diagnosing and treating cardiac, kidney and  
 CC inflammatory diseases associated with inappropriate expression of  
 CC differentially expressed cardiac, kidney and inflammatory genes (e.g.  
 CC AAA46668-79). These genes include I-8U, prostacyclin-stimulating factor,  
 CC isf-2, tissue specific mRNA, insulin-like growth factor binding protein  
 CC 6, OSF-1, gas-1, YMP, BTG2, pre-B cell stimulating factor homologue  
 CC (SDFla), peripheral benzodiazepine receptor, and cellular ligand of  
 CC annexin II (pll), respectively. These diseases include congenital heart  
 CC failure, dilated congestive cardiomyopathy, hypertrophic cardiomyopathy,  
 CC restrictive cardiomyopathy, mitral valve disease, aortic valve disease,  
 CC tricuspid valve disease, angina pectoris, myocardial infarction, cardiac  
 CC arrhythmia, pulmonary hypertension, arterial hypertension, renovascular  
 CC hypertension, arteriosclerosis, atherosclerosis and/or cardiac tumours  
 XX  
 SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 3; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-49;



Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
          |||
Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
          |||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 6

AAB15791

ID AAB15791 standard; protein; 89 AA.

XX

AC AAB15791;

XX

DT 17-JAN-2001 (first entry)

XX

DE Human chemokine SDF1alpha SEQ ID NO: 22.

XX

KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;

KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;

KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;

KW basophil-mediated disease; myocardial infarction; acute ischaemia;

KW rheumatoid arthritis; contraception.

XX

OS Homo sapiens.

XX

PN WO200042071-A2.

XX

PD 20-JUL-2000.

XX

PF 12-JAN-2000; 2000WO-US000821.

XX

PR 12-JAN-1999; 99US-00229071.

PR 17-MAR-1999; 99US-00271192.

PR 01-DEC-1999; 99US-00452406.

XX

PA (NEOR-) NEORX CORP.

XX

PI Grainger DJ, Tatalick LM;

XX

DR WPI; 2000-499101/44.

DR N-PSDB; AAA74883.

XX

PT New peptide 3, amide and heterocyclic compounds and saccharide conjugates

PT used for inhibiting chemokine induced activity and for treating e.g.

PT stroke, vascular diseases, autoimmune diseases and tumor growth.

XX

PS Example 1; Page 134; 387pp; English.

XX

CC The present invention concerns the identification of a number of

CC chemokines which can be used to produce derivatives, agonists and

CC antagonists which are then useful in disease treatment. The chemokines

CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.

CC These chemokine derivatives can be used to treat diseases such as



XX

PA

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Gupta SK;

XX

DR WPI; 2002-697879/75.

DR N-PSDB; ABS53989.

XX

PT Inducing chemotaxis of endothelial cells, useful for regulating  
PT angiogenesis, e.g. for treating cancer, comprises treatment with stromal  
PT cell-derived factor 1 alpha.

XX

PS Claim 1; Fig 2; 26pp; English.

XX

The invention describes a method of inducing chemotaxis of endothelial cells by treatment with stromal cell-derived factor 1alpha (SDF1a). The method is used for stimulating EC chemotaxis, and thus angiogenesis, and is used for treating atherosclerosis, restenosis, ischaemic stroke and spinal cord injury. Inhibition of this process is useful in treatment and prevention of a very wide range of diseases, such as, infection (by bacteria, fungi, protozoa or viruses such as human immunodeficiency virus (HIV) and acquired immunodeficiency syndrome (AIDS)), pain, cancer and benign prostatic hypertrophy, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, anginal pectoris, myocardial infarction, stroke, ulcers, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders (e.g. anxiety, schizophrenia) and dyskinesias (e.g. Huntingdon's disease), inflammatory diseases, rheumatoid arthritis, diabetic retinopathy, inflammatory bowel disease, atherosclerosis, restenosis, Alzheimer's disease, congestive heart failure, cardiac remodeling, angiogenic diseases, solid tumours, and Kaposi Sarcoma. This is the amino acid sequence of human stromal cell derived factor 1-alpha (SDF 1-alpha)

XX

SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 5; Length 89;

Best Local Similarity 100.0%; Pred. No. 1.4e-49;

Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNAKVVVVVLVLVTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Db 1 MNAKVVVVLVLVTALCLSDGKPVLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
| | | | | | | | | | | | | | | | | | | | | |

Db 61 ARLKNNNRQVCIDPKLKWIOEYLEKALNK 89

## RESULT 8

ABG33066

ID    ABG33066 standard; protein; 89 AA.

XX

AC ABG33066;

XX

DT 28-NOV-2002 (first entry)

XX  
DE Human stromal cell derived factor-1a (SDF-1alpha).  
XX  
KW Chemotaxis; endothelial cell; EC; angiogenesis; atherosclerosis;  
KW restenosis; ischaemic stroke; spinal cord injury; infection; bacteria;  
KW fungi; protozoa; virus; pain; cancer; benign prostatic hypertrophy;  
KW diabetes; obesity; anorexia; bulimia; asthma; allergy; hypertension;  
KW Parkinson's disease; acute heart failure; hypotension; urinary retention;  
KW osteoporosis; angina pectoris; myocardial infarction; stroke; dyskinesia;  
KW migraine; vomiting; psychotic disorder; neurological disorder; ulcer;  
KW inflammatory disorder; rheumatoid arthritis; diabetic retinopathy;  
KW inflammatory bowel disease; atherosclerosis; restenosis; Kaposi sarcoma;  
KW Alzheimer's disease; congestive heart failure; cardiac remodelling;  
KW angiogenic disease; solid tumour; human; stromal cell derived factor-1a;  
KW SDF-1alpha.  
XX  
OS Homo sapiens.  
XX  
PN US2002107196-A1.  
XX  
PD 08-AUG-2002.  
XX  
PF 17-SEP-2001; 2001US-00953717.  
XX  
PR 21-JUL-1998; 98US-0093596P.  
PR 21-JUL-1999; 99US-00358624.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Gupta SK;  
XX  
DR WPI; 2002-706230/76.  
DR N-PSDB; ABS53747.  
XX  
PT Inducing chemotaxis of endothelial cells, useful for regulating  
PT angiogenesis, e.g. for treating cancer, comprises treatment with stromal  
PT cell-derived factor 1 alpha.  
XX  
PS Claim 1; Fig 2; 26pp; English.  
XX  
CC The present invention relates to a new method for inducing chemotaxis of  
CC endothelial cells (EC). The method of the invention involves treatment  
CC with a stromal cell-derived factor 1a (SDF1alpha). The method is used for  
CC stimulating EC chemotaxis, and thus angiogenesis, and is used for  
CC treating atherosclerosis, restenosis, ischaemic stroke and spinal cord  
CC injury, while inhibition of this process is useful in treatment and  
CC prevention of a very wide range of diseases, e.g. infection (by bacteria,  
CC fungi, protozoa or viruses), pain, cancer and benign prostatic  
CC hypertrophy, diabetes, obesity, anorexia, bulimia, asthma, allergies,  
CC Parkinson's disease, acute heart failure, hypotension, hypertension,  
CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,  
CC stroke, ulcers, migraine, vomiting, psychotic and neurological disorders  
CC and dyskinesias, inflammatory disorders, rheumatoid arthritis, diabetic  
CC retinopathy, inflammatory bowel disease, atherosclerosis, restenosis,  
CC Alzheimer's disease, congestive heart failure, cardiac remodelling,  
CC angiogenic diseases, solid tumours, and Kaposi sarcoma. The present amino  
CC acid sequence represents the human stromal cell derived factor-1a (SDF-

CC 1alpha) protein of the invention  
XX  
SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 5; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.4e-49;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
|||||  
Db 1 MNAKVVVVLVLVTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
|||||  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 9

ADC78236

ID ADC78236 standard; protein; 89 AA.

XX

AC ADC78236;

XX

DT 01-JAN-2004 (first entry)

XX

DE Human secreted protein SEQ ID NO:43.

XX

KW human; secreted protein; neuroprotective; nootropic; antiparkinsonian;  
KW immunosuppressive; dermatological; antiinflammatory; antirheumatic;  
KW antiarthritic; antithyroid; antianaemic; antidiabetic; hepatotropic;  
KW antiasthmatic; antiallergic; nephrotropic; antiarteriosclerotic;  
KW cardiant; anti-HIV; virucide; antibacterial; fungicide; gynaecological;  
KW cytostatic; gene therapy; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; cardiovascular disorder; renal disorder;  
KW proliferative disorders; cancer; systemic lupus erythematosus;  
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;  
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;  
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;  
KW myocardial infarction; AIDS; infection.

XX

OS Homo sapiens.

XX

PN WO2003072761-A1.

XX

PD 04-SEP-2003.

XX

PF 20-FEB-2003; 2003WO-US004819.

XX

PR 22-FEB-2002; 2002US-0358554P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Birse CE, Komatsoulis G, Choi GH, Olsen H, Ni J, Baker KP;

XX

DR WPI; 2003-721771/68.

DR P-PSDB; ADC78210.



ADW64706

ID ADW64706 standard; protein; 89 AA.

XX

AC ADW64706;

XX

DT 07-APR-2005 (first entry)

XX

DE Human chemokine SDF-1alpha protein sequence SeqID1.

XX

KW chemokine; virucide; anti-HIV; antiinflammatory; immunosuppressive;

KW HIV infection; inflammation; autoimmune disease; veterinary;

KW gene therapy; SDF-1alpha.

XX

OS Homo sapiens.

XX

PN US2005020528-A1.

XX

PD 27-JAN-2005.

XX

PF 23-AUG-2004; 2004US-00924029.

XX

PR 28-FEB-1997; 97US-00808720.

PR 22-OCT-1997; 97US-0113672P.

PR 20-OCT-1998; 98US-00175713.

XX

PA (HERR/) HERRMANN S H.

PA (LUZZ/) LU Z.

PA (MCCO/) MCCOY J M.

PA (SWAN/) SWANBERG S L.

PA (WALK/) WALKER B.

PA (YANG/) YANG O.

XX

PI Herrmann SH, Lu Z, Mccoy JM, Swanberg SL, Walker B, Yang O;

XX

DR WPI; 2005-100856/11.

DR N-PSDB; ADW64708.

XX

PT New composition comprises isolated polynucleotide encoding an amino-terminal-modified chemokine or an amino-terminal-modified chemokine, useful for preventing, treating, or ameliorating HIV infection, inflammatory, or autoimmune condition.

XX

PS Example 1; SEQ ID NO 1; 29pp; English.

XX

CC This invention relates to a novel composition which comprises an isolated  
CC polynucleotide encoding an amino-terminal-modified chemokine or comprises  
CC an amino-terminal-modified chemokine. The invention may be useful for the  
CC production of compounds with a virucide, anti-HIV, antiinflammatory or  
CC immunosuppressive activity. The composition is useful for preventing,  
CC treating, or ameliorating an HIV infection, an inflammatory condition, or  
CC an autoimmune condition. The composition is also useful for veterinary  
CC applications. The amino-terminal-modified chemokine are useful as tolls  
CC for identifying cells expressing receptor for the chemokine, or for  
CC studying binding of chemokine to isolated receptor molecules. They can  
CC also be used as vaccine adjuvants or to affect the chemotactic  
CC recruitment of migratory cells. The polynucleotides can also be used in  
CC gene therapy. The amino-terminal-modified chemokine is a more successful





PT diseases, infectious diseases, AIDS or neuro:degenerative diseases.  
 XX  
 PS Claim 12; Page 26-27; 43pp; English.  
 XX  
 CC A cDNA library prepared from human pro-B cell line FLEB14 cells was  
 CC screened with 32P-labeled mouse SDF-1-alpha cDNA. A positive clone  
 CC contained an insert of 3.5 kb (AAQ74091), including an ORF (AAQ74090)  
 CC encoding human SDF-1-beta (AAR75420). Recombinant hSDF-1-beta was  
 CC produced in E. coli and COS cells  
 XX  
 SQ Sequence 93 AA;

Query Match 100.0%; Score 463; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-49;  
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCP RFFESHVARANVKHLKILNTPNCALQIV 60  
 |||||  
 Db 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCP RFFESHVARANVKHLKILNTPNCALQIV 60  
 Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
 |||||  
 Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 12  
 AAW50766

ID AAW50766 standard; peptide; 93 AA.  
 XX  
 AC AAW50766;  
 XX  
 DT 27-JUL-1998 (first entry)  
 XX  
 DE Human SDF-1 which is useful for treating HIV.  
 XX  
 KW Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus; HIV;  
 KW CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN FR2751658-A1.  
 XX  
 PD 30-JAN-1998.  
 XX  
 PF 26-JUL-1996; 96FR-00009477.  
 XX  
 PR 26-JUL-1996; 96FR-00009477.  
 XX  
 PA (INSP ) INST PASTEUR.  
 XX  
 PI Arenzana SF, Virelizier JL, Baggiolini M, Moser B, Clark LI;  
 XX  
 DR WPI; 1998-123039/12.  
 DR P-PSDB; AAV07076.  
 XX  
 PT Human stromal cell-derived chemokine, SDF-1 - useful for treating human  
 PT immunodeficiency virus infection.

XX  
 PS Claim 4; Fig 5; 48pp; French.  
 XX  
 CC The invention relates to peptides which bind to a cellular receptor for  
 CC CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-  
 CC expressed transmembrane domain receptor), especially where the peptide is  
 CC human chemokine SDF-1. The peptide can be used to treat or prevent HIV  
 CC infections, optionally together with reverse transcriptase inhibitors,  
 CC viral protease inhibitors, soluble CD4 receptors, CD4 receptor  
 CC antagonists, immunotherapy agents, agents for treating HIV- associated  
 CC opportunistic infections and/or other CXC or CC chemokines, especially  
 CC RANTES, MIP1- alpha , MIP1- beta or MCP1. The peptide can be used to  
 CC detect anti-SDF-1 antibodies in biological fluids. This sequence  
 CC represents human SDF-1  
 XX  
 SQ Sequence 93 AA;

Query Match 100.0%; Score 463; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-49;  
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
 |||||  
 Db 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
 Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
 |||||  
 Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

# RESULT 13

AAY26178

ID AAY26178 standard; protein; 93 AA.

XX

AC AAY26178;

XX

DT 29-SEP-1999 (first entry)

XX

DE Stromal cell derived factor 1b.

XX

KW Stromal cell derived factor 1b; SDF 1b; vaccine; immune response;

KW antigen; humoral response; cell-mediated response; PCR;

KW immunostimulatory; expression plasmid vector.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .21

FT /note= "Signal peptide"

FT Protein 22. .93

FT /label= SDF\_1b

FT /note= "Stromal cell-derived factor 1b"

XX

PN W09929728-A1.

XX

PD 17-JUN-1999.

XX

PF 11-DEC-1998; 98WO-US026291.  
 XX  
 PR 11-DEC-1997; 97US-0069281P.  
 XX  
 PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.  
 XX  
 PI Gallo RC, Devico AL, Garzino-Demo A;  
 XX  
 DR WPI; 1999-385578/32.  
 DR N-PSDB; AAX80633.  
 XX  
 PT Methods of enhancing vaccine efficacy.  
 XX  
 PS Claim 4; Page 103; 134pp; English.  
 XX  
 CC The present sequence is stromal cell derived factor-1b. This belongs to  
 CC the CXC class of chemokines. This is chemotactic for mature dendritic  
 CC cells. The efficacy of a vaccine is enhanced by combining it with one or  
 CC more chemokines to enhance the immune response to an antigen. This can be  
 CC humoral or cell-mediated immune response. The purified chemokines,  
 CC fragments, derivatives or analogues are administered either concurrently  
 CC with one or more purified antigens against which an immune response is  
 CC desired or within a time period either before or after antigen  
 CC administration. The chemokine gene is isolated by PCR, and administered  
 CC by constructing an expression plasmid vector which can be expressed in a  
 CC coordinated manner upon introduction in a suitable cell. The vaccines are  
 CC immunostimulatory and can be used to treat microbial diseases especially  
 CC HIV  
 XX  
 SQ Sequence 93 AA;

Query Match 100.0%; Score 463; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-49;  
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
  
 Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
 ||||||||||||||||||||||||||||||||  
 Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

#### RESULT 14

AA06725

ID AAY06725 standard; protein; 93 AA.

XX

AC AAY06725;

XX

DT 18-JUN-1999 (first entry)

XX

DE Amino acid sequence of native SDF-1 alpha.

XX

KW Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;  
 KW infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; vMIP;  
 KW allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPAV;

KW stromal cell derived factor 1; Macrophage Inflammatory protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9911655-A1.  
 XX  
 PD 11-MAR-1999.  
 XX  
 PF 31-AUG-1998; 98WO-US018096.  
 XX  
 PR 04-SEP-1997; 97US-0057620P.  
 XX  
 PA (GRYP-) GRYPHON SCI.  
 XX  
 PI Kent SBH, Siani MA, Simon R, Wilken J;  
 XX  
 DR WPI; 1999-205128/17.  
 XX  
 PT New cross-over proteins for treatment of inflammation and infections e.g.  
 PT AIDS - prepared by ligation of two functional protein modules derived  
 PT from two different parent molecules.  
 XX  
 PS Example 4; Page 41; 75pp; English.  
 XX  
 CC The invention relates to a cross-over protein produced by chemical  
 CC ligation of at least two functional protein modules derived from at least  
 CC two parent protein molecules. The cross-over proteins can be used in  
 CC pharmaceutical compositions for therapy of inflammatory and infectious  
 CC diseases including AIDS, and for indications of hematopoiesis and  
 CC chemoprotection. They are also useful for treatment of asthma, allergic  
 CC rhinitis, atopic dermatitis and rheumatoid arthritis. A library  
 CC comprising a collection of cross-over proteins is useful for screening  
 CC for cross-over proteins that are receptor ligands. The libraries comprise  
 CC functionally diverse compounds therefore improving the drug discovery  
 CC process. The proteins and libraries are exemplified by the preparation of  
 CC cross-over chemokines comprising various combinations of peptide segments  
 CC derived from RANTES, SDF-1 (stromal cell derived factor 1), vMIP (viral  
 CC Macrophage Inflammatory protein) and other such chemokines. The present  
 CC sequence represents a native amino acid fragment of SDF-1 alpha  
 XX  
 SQ Sequence 93 AA;

Query Match 100.0%; Score 463; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-49;  
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
 Qy 61 ARLKNNNRQVCIDPKLKWIEYLEKALNK 89  
 ||||||||||||||||||||||||  
 Db 61 ARLKNNNRQVCIDPKLKWIEYLEKALNK 89

RESULT 15  
 AAB15812

ID AAB15812 standard; protein; 93 AA.  
 XX  
 AC AAB15812;  
 XX  
 DT 17-JAN-2001 (first entry)  
 XX  
 DE Human chemokine SDF1beta SEQ ID NO: 56.  
 XX  
 KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;  
 KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;  
 KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;  
 KW basophil-mediated disease; myocardial infarction; acute ischaemia;  
 KW rheumatoid arthritis; contraception.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200042071-A2.  
 XX  
 PD 20-JUL-2000.  
 XX  
 PF 12-JAN-2000; 2000WO-US000821.  
 XX  
 PR 12-JAN-1999; 99US-00229071.  
 PR 17-MAR-1999; 99US-00271192.  
 PR 01-DEC-1999; 99US-00452406.  
 XX  
 PA (NEOR-) NEORX CORP.  
 XX  
 PI Grainger DJ, Tatalick LM;  
 XX  
 DR WPI; 2000-499101/44.  
 DR N-PSDB; AAA74869.  
 XX  
 PT New peptide 3, amide and heterocyclic compounds and saccharide conjugates  
 PT used for inhibiting chemokine induced activity and for treating e.g.  
 PT stroke, vascular diseases, autoimmune diseases and tumor growth.  
 XX  
 PS Disclosure; Page 366; 387pp; English.  
 XX  
 CC The present invention concerns the identification of a number of  
 CC chemokines which can be used to produce derivatives, agonists and  
 CC antagonists which are then useful in disease treatment. The chemokines  
 CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.  
 CC These chemokine derivatives can be used to treat diseases such as  
 CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and  
 CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated  
 CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and  
 CC rheumatoid arthritis, and can be used to prevent strokes and as  
 CC contraceptives. The coding sequences for the chemokines can be used in  
 CC gene therapy for the same diseases, as well as in the production of  
 CC animal models  
 XX  
 SQ Sequence 93 AA;

Query Match 100.0%; Score 463; DB 3; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-49;  
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 26, 2006, 02:33:39  
Job time : 190 secs

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2006, 02:33:59 ; Search time 38 Seconds  
 (without alignments)  
 225.350 Million cell updates/sec

Title: US-10-785-230-5  
 Perfect score: 463  
 Sequence: 1 MNAKVVVVLVLVTALCLSD.....VCIDPKLKWIQEYLEKALNK 89

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_80:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	463	100.0	93	2	G01540	cytokine SDF-1-bet
2	442	95.5	89	2	I53416	interleukin-8 homo
3	442	95.5	89	2	A53497	pre-B-cell growth-
4	442	95.5	93	2	I81182	cytokine - mouse
5	113.5	24.5	101	2	I48148	Neutrophil attract
6	113	24.4	99	2	A37034	interleukin-8 prec
7	112.5	24.3	96	2	A32954	gro-alpha precurs
8	111	24.0	95	2	JN0841	interleukin-8 - do
9	111	24.0	98	2	I59277	Mob-1 - rat
10	110	23.8	103	2	A26736	transformation-ind
11	108	23.3	103	2	I50417	RSV-induced protei
12	107	23.1	101	2	S42496	interleukin-8 prec
13	106.5	23.0	91	1	A28815	monocyte chemoattr

14	106.5	23.0	91	1	A46539	monocyte chemoattr
15	106.5	23.0	101	2	B28414	growth-regulated p
16	104.5	22.6	100	2	JH0200	macrophage inflammm
17	103.5	22.4	107	2	B38290	GRO-gamma precurs
18	102.5	22.1	100	2	I55614	macrophage inflammm
19	102.5	22.1	100	2	S21467	macrophage inflammm
20	102	22.0	101	2	I46871	interleukin-8 - ra
21	101.5	21.9	96	2	JN0572	neutrophil chemo-a
22	100.5	21.7	107	2	JH0281	macrophage inflammm
23	99	21.4	98	2	A45492	IP-10 precursor -
24	98.5	21.3	120	2	JE0177	lymphocyte and mon
25	98	21.2	103	2	A53096	interleukin-8 prec
26	97	21.0	119	2	S42881	platelet basic pro
27	96.5	20.8	107	2	A28414	melanoma growth-st
28	96.5	20.8	120	2	I48147	monocyte chemoattr
29	95	20.5	148	1	S07723	immediate-early se
30	94.5	20.4	92	2	I52322	macrophage inflammm
31	94.5	20.4	128	1	TGHU	beta-thromboglobul
32	93	20.1	109	2	A54678	monocyte chemotact
33	87.5	18.9	126	2	A35766	platelet factor 4,
34	86	18.6	98	1	TGHUGI	interferon gamma-i
35	86	18.6	100	2	S46198	cytokine-induced n
36	84.5	18.3	148	1	A30209	PDGF-inducible JE
37	84	18.1	75	2	A54188	granulocyte chemot
38	83.5	18.0	114	2	A55010	neutrophil-activat
39	83	17.9	117	2	B44253	alveolar macrophag
40	83	17.9	125	2	JN0470	interferon gamma-i
41	82.5	17.8	132	2	A57325	C-X-C chemokine LI
42	82	17.7	113	2	JC7800	neutrophil activat
43	82	17.7	870	2	A41130	dystrophin homolog
44	81.5	17.6	75	2	B54188	granulocyte chemot
45	79	17.1	92	2	I46730	immune activation

#### ALIGNMENTS

##### RESULT 1

G01540

cytokine SDF-1-beta - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004

C;Accession: G01540

R;Spotila, L.D.

submitted to the EMBL Data Library, October 1994

A;Reference number: G07697

A;Accession: G01540

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-93 <SPO>

A;Cross-references: UNIPROT:P48061; UNIPARC:UPI000003092F; EMBL:U16752;

NID:g1272194; PID:g571508

C;Superfamily: beta-thromboglobulin

Query Match 100.0%; Score 463; DB 2; Length 93;

Best Local Similarity 100.0%; Pred. No. 4.2e-45;

Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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Qy      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIV 60
        |||
Db      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
        |||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

```

T53416

C;Species: Mus sp. (mouse)

C;Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text change 05-Nov-1999

C;Accession: I53416

R; Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.

Exp. Cell Res. 215, 284-293, 1994

Ar>Title: Molecular cloning of TPAR1, a gene whose expression is repressed by the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).

A:Reference number: I53416; MUID:95073497; PMID:7982471

A;Accession: I53416

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-89 <RES>

A;Cross-references: UNIPARC:UPI00000018A3; GB:S74318; NID:q786393;

PIDN:AAB32650.1; PID:q786394

C;Genetics:

A;Gene: TPAR1

C;Superfamily: beta-thromboglobulin

Query Match 95.5%; Score 442; DB 2; Length 89;  
Best Local Similarity 93.3%; Pred. No. 9.5e-43;  
Matches 83; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

Qy      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
      |:|||| || || ||||:|||||||:|||||||
Db      1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHIARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
      |||||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

```

A53497

pre-B-cell growth-stimulating factor precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence revision 02-Jun-1994 #text change 09-Jul-2004

C;Accession: A53497; I59582

R; Nagasawa, T.; Kikutani, H.; Kishimoto, T.

Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994

A;Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.

A;Reference number: A53497; MUID:94181581; PMID:8134392

A;Accession: A53497

A;Status: preliminary

A;Molecule type: mRNA  
A;Residues: 1-89 <NAG>  
A;Cross-references: UNIPROT:P40224; UNIPARC:UPI00000018A3; GB:D21072;  
NID:g413905; PIDN:BAA04648.1; PID:g468457  
R;Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.  
Science 261, 600-603, 1993  
A;Title: Signal sequence trap: a cloning strategy for secreted proteins and type  
I membrane proteins.  
A;Reference number: I59582; MUID:93342488; PMID:8342023  
A;Accession: I59582  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-89 <RES>  
A;Cross-references: UNIPARC:UPI00000018A3; GB:L12029; NID:g393179;  
PIDN:AAA40100.1; PID:g393180  
C;Genetics:  
A;Gene: SDF-1-alpha  
C;Superfamily: beta-thromboglobulin  
C;Keywords: cytokine

Query Match 95.5%; Score 442; DB 2; Length 89;  
Best Local Similarity 93.3%; Pred. No. 9.5e-43;  
Matches 83; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60  
|:|||| || ||| |||:|||||||:|||||||  
Db 1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHIARANVKHLKILNTPNCALQIV 60  
Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
|:|||||  
Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

#### RESULT 4

I81182

cytokine - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004

C;Accession: I81182

R;Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.  
Science 261, 600-603, 1993

A;Title: Signal sequence trap: a cloning strategy for secreted proteins and type  
I membrane proteins.

A;Reference number: I59582; MUID:93342488; PMID:8342023

A;Accession: I81182

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-93 <RES>

A;Cross-references: UNIPROT:P40224; UNIPARC:UPI000002A125; GB:L12030;

NID:g393181; PIDN:AAA40101.1; PID:g393182

C;Genetics:

A;Gene: SDF-1-beta

C;Superfamily: beta-thromboglobulin

Query Match 95.5%; Score 442; DB 2; Length 93;  
Best Local Similarity 93.3%; Pred. No. 9.9e-43;  
Matches 83; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

Qy      1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
      |:|||| || ||| |||:||||||||||||||||||:||||||||||||||||||
Db      1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHIARANVKHLKILNTPNCALQIV 60

Qy      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
      ||||||||||||||||||||||||||||||||
Db      61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

```

# RESULT 5

I48148

Neutrophil attractant protein-1 - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I48148

R;Yoshimura, T.; Johnson, D.G.

J. Immunol. 151, 6225-6236, 1993

A;Title: cDNA cloning and expression of guinea pig neutrophil attractant protein-1 (NAP-1): NAP-1 is highly conserved in guinea pig.

A;Reference number: I48148; MUID:94065176; PMID:7504015

A;Accession: I48148

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-101 <RES>

A;Cross-references: UNIPROT:P49113; UNIPARC:UPI000012D4F8; GB:L04986;

NID:g459764; PIDN:AAA37049.1; PID:g459765

C;Genetics:

A;Gene: NAP-1

C;Superfamily: beta-thromboglobulin

```

Query Match          24.5%;  Score 113.5;  DB 2;  Length 101;
Best Local Similarity 32.6%;  Pred. No. 1.3e-05;
Matches 30;  Conservative 20;  Mismatches 31;  Indels 11;  Gaps 6;

```

```

Qy      6 VVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARAN--VKHLKILNT-PNCA-L 57
      | || | | : | : | | : | | : | | : | | : | |
Db      7 VAVLAAFLLSAVLCEGMVVTKLVSELRCQC--IKIHTTFFHPKFIKELKVIESGPRCANS 64

Qy      58 QIVARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
      :| :| :|||:|:| | ||:| : | :
Db      65 EIIIVKL-SDNRQLCLDPKKKWVQDVVSMFLKR 95

```

# RESULT 6

A37034

interleukin-8 precursor - human

N;Alternate names: beta-thromboglobulin-like protein; fibroblast-derived

neutrophil-activating factor alpha; lung carcinoma-derived chemotaxin;

lymphocyte-derived neutrophil-activating factor; monocyte-derived neutrophil

chemotactic factor; monocyte-derived neutrophil-activating factor

C;Species: Homo sapiens (man)

C;Date: 08-Dec-1992 #sequence\_revision 08-Dec-1992 #text\_change 09-Jul-2004

C;Accession: A37034; JI0041; A32791; S37634; PL0107; A28598; A27488; A39960;

A60401; A60591; S15827; S04216; A60567; A60847; S15417; S03975; I54560; I55992;

I37902; S67519

R;Mukaida, N.; Shiroo, M.; Matsushima, K.

J. Immunol. 143, 1366-1371, 1989  
A;Title: Genomic structure of the human monocyte-derived neutrophil chemotactic factor IL-8.  
A;Reference number: A37034; MUID:89309826; PMID:2663993  
A;Accession: A37034  
A;Molecule type: DNA  
A;Residues: 1-99 <MUK>  
A;Cross-references: UNIPROT:P10145; UNIPARC:UPI0000000DD0; GB:M28130; NID:g186367; PIDN:AAA59158.1; PID:g186368  
A;Note: the authors failed to translate the last thirty-six nucleotides of the second exon  
R;Matsushima, K.; Morishita, K.; Yoshimura, T.; Lavu, S.; Kobayashi, Y.; Lew, W.; Appella, E.; Kung, H.F.; Leonard, E.J.; Oppenheim, J.J.  
J. Exp. Med. 167, 1883-1893, 1988  
A;Title: Molecular cloning of a human monocyte-derived neutrophil chemotactic factor (MDNCF) and the induction of MDNCF mRNA by interleukin 1 and tumor necrosis factor.  
A;Reference number: JL0041; MUID:88258376; PMID:3260265  
A;Accession: JL0041  
A;Molecule type: mRNA  
A;Residues: 1-99 <MA1>  
A;Cross-references: UNIPARC:UPI0000000DD0; EMBL:Y00787; NID:g34518; PIDN:CAA68742.1; PID:g34519  
A;Note: the sequence shows similarity to several platelet-derived factors, a v-src-induced protein, a growth-regulated gene product (gro), and an IFN-gamma-inducible protein  
R;Kowalski, J.; Denhardt, D.T.  
Mol. Cell. Biol. 9, 1946-1957, 1989  
A;Title: Regulation of the mRNA for monocyte-derived neutrophil-activating peptide in differentiating HL60 promyelocytes.  
A;Reference number: A32791; MUID:89313739; PMID:2664463  
A;Accession: A32791  
A;Molecule type: mRNA  
A;Residues: 1-99 <KOW>  
A;Cross-references: UNIPARC:UPI0000000DD0; GB:M26383; NID:g188627; PIDN:AAA36323.1; PID:g188628  
R;King, C.H.; Gordon, G.S.; Konieczkowski, M.; Sedor, J.R.  
submitted to the EMBL Data Library, February 1992  
A;Reference number: S37634  
A;Accession: S37634  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-97 <KIN>  
A;Cross-references: UNIPARC:UPI000000077C; EMBL:Z11686; NID:g33958; PIDN:CAA77745.1; PID:g33959  
R;Suzuki, K.; Miyasaka, H.; Ota, H.; Yamakawa, Y.; Tagawa, M.; Kuramoto, A.; Mizuno, S.  
J. Exp. Med. 169, 1895-1901, 1989  
A;Title: Purification and partial primary sequence of a chemotactic protein for polymorphonuclear leukocytes derived from human lung giant cell carcinoma LU65C cells.  
A;Reference number: PL0107; MUID:89279141; PMID:2659722  
A;Accession: PL0107  
A;Molecule type: protein  
A;Residues: 23-32, 'XR', 35, 'X', 37-52, 'L', 54 <SUZ>  
A;Cross-references: UNIPARC:UPI0000177BEA  
A;Experimental source: lung giant cell carcinoma LU65C

R;Gregory, H.; Young, J.; Schroeder, J.M.; Mrowietz, U.; Christophers, E.  
 Biochem. Biophys. Res. Commun. 151, 883-890, 1988  
 A;Title: Structure determination of a human lymphocyte derived neutrophil  
 activating peptide (LYNAP).  
 A;Reference number: A28598; MUID:88162914; PMID:3279957  
 A;Accession: A28598  
 A;Molecule type: protein  
 A;Residues: 28-99 <GRE>  
 A;Cross-references: UNIPARC:UPI000003094C  
 R;Walz, A.; Peveri, P.; Aschauer, H.; Baggiolini, M.  
 Biochem. Biophys. Res. Commun. 149, 755-761, 1987  
 A;Title: Purification and amino acid sequencing of NAF, a novel neutrophil-  
 activating factor produced by monocytes.  
 A;Reference number: A27488; MUID:88106502; PMID:3322281  
 A;Accession: A27488  
 A;Molecule type: protein  
 A;Residues: 28-59 <WAL>  
 A;Cross-references: UNIPARC:UPI0000177BEB  
 R;Yoshimura, T.; Matsushima, K.; Tanaka, S.; Robinson, E.A.; Appella, E.;  
 Oppenheim, J.J.; Leonard, E.J.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 9233-9237, 1987  
 A;Title: Purification of a human monocyte-derived neutrophil chemotactic factor  
 that has peptide sequence similarity to other host defense cytokines.  
 A;Reference number: A39960; MUID:88097462; PMID:3480540  
 A;Accession: A39960  
 A;Molecule type: protein  
 A;Residues: 28-69 <YOS>  
 A;Cross-references: UNIPARC:UPI0000177BEC  
 R;Schroeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.;  
 Christophers, E.  
 J. Immunol. 144, 2223-2232, 1990  
 A;Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three  
 NAP-1/IL-8-related neutrophil chemotactic proteins in human dermal fibroblasts.  
 A;Reference number: A60401; MUID:90187866; PMID:2179408  
 A;Accession: A60401  
 A;Molecule type: protein  
 A;Residues: 23-32 <SCH>  
 A;Cross-references: UNIPARC:UPI0000158437  
 A;Experimental source: dermal fibroblasts  
 A;Note: a minor component of this material (15%) includes an additional two  
 amino acids at the amino end  
 R;Van Damme, J.; Decock, B.; Conings, R.; Lenaerts, J.P.; Opdenakker, G.;  
 Billiau, A.  
 Eur. J. Immunol. 19, 1189-1194, 1989  
 A;Title: The chemotactic activity for granulocytes produced by virally infected  
 fibroblasts is identical to monocyte-derived interleukin 8.  
 A;Reference number: A60591; MUID:89338542; PMID:2668011  
 A;Accession: A60591  
 A;Molecule type: protein  
 A;Residues: 23-33,'X',35,'X',37-42 <VAN>  
 A;Cross-references: UNIPARC:UPI000006F8F7  
 R;Nakagawa, H.; Hatakeyama, S.; Ikesue, A.; Miyai, H.  
 FEBS Lett. 282, 412-414, 1991  
 A;Title: Generation of interleukin-8 by plasmin from AVLPR-interleukin-8, the  
 human fibroblast-derived neutrophil chemotactic factor.  
 A;Reference number: S15827; MUID:91243843; PMID:1828038  
 A;Accession: S15827

A;Molecule type: protein  
 A;Residues: 23-33,'X',35,'X',37-47 <FEB>  
 A;Cross-references: UNIPARC:UPI000006D6FA  
 R;van Damme, J.; van Beeumen, J.; Conings, R.; Decock, B.; Billiau, A.  
 Eur. J. Biochem. 181, 337-344, 1989  
 A;Title: Purification of granulocyte chemotactic peptide/interleukin-8 reveals N-terminal sequence heterogeneity similar to that of beta-thromboglobulin.  
 A;Reference number: S04216; MUID:89231715; PMID:2523801  
 A;Accession: S04216  
 A;Molecule type: protein  
 A;Residues: 21-67 <VA2>  
 A;Cross-references: UNIPARC:UPI0000177BED  
 R;Yoshimura, T.; Robinson, E.A.; Appella, E.; Matsushima, K.; Showalter, S.D.; Skeel, A.; Leonard, E.J.  
 Mol. Immunol. 26, 87-93, 1989  
 A;Title: Three forms of monocyte-derived neutrophil chemotactic factor (MDNCF) distinguished by different lengths of the amino-terminal sequence.  
 A;Reference number: A60567; MUID:89181632; PMID:2648135  
 A;Accession: A60567  
 A;Molecule type: protein  
 A;Residues: 21-33,'X',35,'X',37-47 <YO2>  
 A;Cross-references: UNIPARC:UPI0000177BEE  
 A;Note: the forms starting from positions 21, 23, and 28 represented 8%, 47%, and 45%, respectively, of total interleukin-8  
 R;Van Damme, J.; Van Beeumen, J.; Opdenakker, G.; Billiau, A.  
 J. Exp. Med. 167, 1364-1376, 1988  
 A;Title: A novel, NH-2-terminal sequence-characterized human monokine possessing neutrophil chemotactic, skin-reactive, and granulocytosis-promoting activity.  
 A;Reference number: A60847; MUID:88187604; PMID:3258625  
 A;Accession: A60847  
 A;Molecule type: protein  
 A;Residues: 28-47 <VA3>  
 A;Cross-references: UNIPARC:UPI0000177BEF  
 R;Car, B.D.; Baggiolini, M.; Walz, A.  
 Biochem. J. 275, 581-584, 1991  
 A;Title: Formation of neutrophil-activating peptide 2 from platelet-derived connective-tissue-activating peptide III by different tissue proteinases.  
 A;Reference number: S15417; MUID:91248085; PMID:2039437  
 A;Accession: S15417  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 28-99 <CAR>  
 A;Cross-references: UNIPARC:UPI000003094C  
 R;Golds, E.E.; Mason, P.; Nyirkos, P.  
 Biochem. J. 259, 585-588, 1989  
 A;Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a neutrophil chemotactic factor but not beta-2--microglobulin in human synovial cells and fibroblasts.  
 A;Reference number: S03975; MUID:89246368; PMID:2655583  
 A;Accession: S03975  
 A;Molecule type: protein  
 A;Residues: 23-46 <GOL>  
 A;Cross-references: UNIPARC:UPI0000177BF0  
 R;Hotta, K.; Hayashi, K.; Ishikawa, J.; Tagawa, M.; Hashimoto, K.; Mizumo, S.; Suzuki, K.  
 Immunol. Lett. 24, 165-170, 1990

A;Title: Coding region structure of interleukin-8 gene of human lung giant cell carcinoma LU65C cells that produce LUCT/interliukin-8: homogeneity in interleuki-8 genes.  
 A;Reference number: I54560; MUID:90346419; PMID:2200751  
 A;Accession: I54560  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-99 <RES>  
 A;Cross-references: UNIPARC:UPI0000000DD0; GB:D14283; NID:g219915; PIDN:BAA03245.1; PID:g219916  
 R;Schmid, J.; Weissmann, C.  
 J. Immunol. 139, 250-256, 1987  
 A;Title: Induction of mRNA for a serine protease and a beta-thromboglobulin-like protein in mitogen-stimulated human leukocytes.  
 A;Reference number: I55992; MUID:87224164; PMID:2953813  
 A;Accession: I55992  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-99 <RE2>  
 A;Cross-references: UNIPARC:UPI0000000DD0; GB:M17017; NID:g179579; PIDN:AAA35611.1; PID:g179580  
 R;Kusner, D.J.; Luebbers, E.L.; Nowinski, R.J.; Konieczkowski, M.; King, C.H.; Sedor, J.R.  
 Kidney Int. 39, 1240-1248, 1991  
 A;Title: Cytokine- and LPS-induced synthesis of interleukin-8 from human mesangial cells.  
 A;Reference number: I37902; MUID:91374977; PMID:1895676  
 A;Accession: I37902  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-97 <RE3>  
 A;Cross-references: UNIPARC:UPI000000077C; EMBL:Z11686; NID:g33958; PIDN:CAA77745.1; PID:g33959  
 R;Alouani, S.; Gaertner, H.F.; Mermoud, J.J.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.; Proudfoot, A.E.I.  
 Eur. J. Biochem. 227, 328-334, 1995  
 A;Title: A fluorescent interleukin-8 receptor probe produced by targetted labelling at the amino terminus.  
 A;Reference number: S67519; MUID:95154308; PMID:7851404  
 A;Accession: S67519  
 A;Molecule type: mRNA  
 A;Residues: 1-99 <ALO>  
 A;Cross-references: UNIPARC:UPI0000000DD0  
 C;Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes.  
 C;Comment: This protein is variably processed at the amino end. The major form differs in different cell types.  
 C;Genetics:  
 A;Gene: GDB:IL8  
 A;Cross-references: GDB:120099; OMIM:146930  
 A;Map position: 4q13-4q21  
 A;Introns: 22/1; 67/2; 95/2  
 C;Superfamily: beta-thromboglobulin  
 C;Keywords: chemotaxis; cytokine; inflammation  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-99/Product: interleukin-8, minor form #status experimental <MATA>





Qy 10 VLVLTA LCS DGKPVSLSYRCPCRFFESHVARANVKHLKIL-NTPNCA-LQIVARLKNNN 67  
 :|:| | : | |:: || | : : |:: ||:| : |:| ::| || |  
 Db 13 LLLLATSR LATGAPIANELRCQCLQTMAGIHLKNIQSLKVLPSGPHCTQTEVIATLK-NG 71  
 Qy 68 RQVCIDPKLKWIQEYLEKAL 87  
 |: |::| : |: ::| |  
 Db 72 REACLDPEAPLVQKIVQKML 91

# RESULT 8

JN0841

interleukin-8 - dog

C;Species: Canis lupus familiaris (dog)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 12-Apr-1995

C;Accession: JN0841

R;Ishikawa, J.; Suzuki, S.; Hotta, K.; Hirota, Y.; Mizuno, S.; Suzuki, K.

Gene 131, 305-306, 1993

A;Title: Cloning of a canine gene homologous to the human interleukin-8-encoding gene.

A;Reference number: JN0841; MUID:94010328; PMID:7916715

A;Accession: JN0841

A;Molecule type: DNA

A;Residues: 1-95 <ISH>

A;Cross-references: UNIPARC:UPI0000177BDC

C;Comment: This protein is a polymorphonuclear leukocytes chemotactic factor and is involved in the host defense function.

C;Genetics:

A;Introns: 22/1; 67/2

C;Superfamily: beta-thromboglobulin

Query Match 24.0%; Score 111; DB 2; Length 95;  
 Best Local Similarity 33.7%; Pred. No. 2.3e-05;  
 Matches 34; Conservative 20; Mismatches 29; Indels 18; Gaps 7;

Qy 1 MNAKVVVVLV---LVLTA LCS DGKPVSLSYRCPCRFFESHVARANVKHLKILNT- 52  
 | :|: | |: :: ||| || || || | :| : |:| |  
 Db 1 MTSKLAVALLAA FVLSAALCEAAVLS---RVSSELRCQC--IKTHSTPFHHPKYIKELRVI 55  
 Qy 53 ---PNCA-LQIVARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
 |:| :|: :| | | :||:|||| ||:|: :: | |  
 Db 56 DSGPHCENSEIIVKLENGN-EVCLDPKEKWWQKVQIFLKK 95

# RESULT 9

I59277

Mob-1 - rat

C;Species: Rattus sp. (rat)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999

C;Accession: I59277

R;Liang, P.; Averboukh, L.; Zhu, W.; Pardee, A.B.

Proc. Natl. Acad. Sci. U.S.A. 91, 12515-12519, 1994

A;Title: Ras activation of genes: Mob-1 as a model.

A;Reference number: I59277; MUID:95107988; PMID:7809069

A;Accession: I59277

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-98 <RES>  
A;Cross-references: UNIPARC:UPI0000136774; EMBL:U17035; NID:g763535;  
PIDN:AAB60485.1; PID:g602432  
C;Genetics:  
A;Gene: mob-1  
C;Superfamily: beta-thromboglobulin

Query Match 24.0%; Score 111; DB 2; Length 98;  
Best Local Similarity 33.0%; Pred. No. 2.4e-05;  
Matches 31; Conservative 22; Mismatches 33; Indels 8; Gaps 4;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARAN-VKHLKI----LNTPNC 55  
|| ||| ||| :| :| |:: :|| | | : |:| |:| :|  
Db 1 MNPSAAVVLCLVLLSLSGTQGIPLARTVRCCTCIDFHEQTLRPRAIGKLEIIPASLSCPH- 59  
  
Qy 56 ALQIVARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
::|:| :| || :|::|: :|: | ||:::  
Db 60 -VEIIATMKKNNEKRCINPESEAIKSLK-KAVSQ 91

#### RESULT 10

A26736

transformation-induced protein precursor (clone 9E3) - chicken

C;Species: Gallus gallus (chicken)

C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 09-Jul-2004

C;Accession: A26736

R;Sugano, S.; Stoeckle, M.Y.; Hanafusa, H.

Cell 49, 321-328, 1987

A;Title: Transformation by Rous sarcoma virus induces a novel gene with homology to a mitogenic platelet protein.

A;Reference number: A26736; MUID:87187628; PMID:3032449

A;Accession: A26736

A;Molecule type: mRNA

A;Residues: 1-103 <SUG>

A;Cross-references: UNIPROT:P08317; UNIPARC:UPI000000031A; GB:M16199;

NID:g211735; PIDN:AAA48758.1; PID:g211736

C;Superfamily: beta-thromboglobulin

C;Keywords: growth factor

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-103/Product: transformation-induced protein #status predicted <MAT>

Query Match 23.8%; Score 110; DB 2; Length 103;  
Best Local Similarity 32.3%; Pred. No. 3.2e-05;  
Matches 30; Conservative 23; Mismatches 32; Indels 8; Gaps 6;

Qy 1 MNAKVVVVLVLVLTALCLSDGKP-VLSYRCPCRFFESH---VARANVKHLKIL-NTPNC 55  
|| |: || |:| : || |: | : |: :| : :: :|: : |:|  
Db 1 MNGKLGAVLALLLVSAALSQGRTLVKMGNELRCQCISTHSKFIHPKSIQDVKLTPSGPHC 60  
  
Qy 56 A-LQIVARLKNNNRQVCIDPKLKWIQEYLEKAL 87  
::|:| || :|:|:| | :| : |||  
Db 61 KNVEIIATLK-DGREVCLDPTAPWVQ-LIVKAL 91

#### RESULT 11

I50417

RSV-induced protein - chicken

C;Species: Gallus gallus (chicken)  
 C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
 C;Accession: I50417  
 R;Bedard, P.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 6715-6719, 1987  
 A;Title: Constitutive expression of a gene encoding a polypeptide homologous to biologically active human platelet protein in Rous sarcoma virus-transformed fibroblasts virus transformed fibroblasts.  
 A;Reference number: I50417; MUID:88016162; PMID:2821543  
 A;Accession: I50417  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-103 <BED>  
 A;Cross-references: UNIPROT:P08317; UNIPARC:UPI00001713A9; GB:J02975; NID:g212643; PIDN:AAA49059.1; PID:g212644  
 C;Superfamily: beta-thromboglobulin

Query Match 23.3%; Score 108; DB 2; Length 103;  
 Best Local Similarity 32.3%; Pred. No. 5.4e-05;  
 Matches 30; Conservative 22; Mismatches 33; Indels 8; Gaps 6;

Qy 1 MNAKVVVVLVLVLTALCLSDGKP-VLSYRCPCRFFESH---VARANVKHLKIL-NTPNC 55  
 || | || |:| : || |: | : |: |:| : :: |: |:|  
 Db 1 MNGKFGAVLALLVSAALSQGRTLVKMGNELRCQCISTHSKFIHPKSIQDVKLTPSGPHC 60  
 Qy 56 A-LQIVARLKNNNRQVCIDPKLKWIQEYLEKAL 87  
 ::|:| || : |:|:| | |:| : |||  
 Db 61 KNVEIIATLK-DGREVCLDPTAPWVQ-LIVKAL 91

RESULT 12  
 S42496

interleukin-8 precursor [similarity] - sheep  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C;Accession: S42496; I46997  
 R;Legastelois, I.; Greenland, T.; Arnaud, P.; Mornex, J.F.; Cordier, G.  
 submitted to the EMBL Data Library, March 1994  
 A;Description: Nucleotide sequence of ovine interleukin 8 cDNA using polymerase chain reaction.  
 A;Reference number: S42496  
 A;Accession: S42496  
 A;Molecule type: mRNA  
 A;Residues: 1-101 <LEG>  
 A;Cross-references: UNIPROT:P36925; UNIPARC:UPI000012D4FE; EMBL:X78306; NID:g463253; PIDN:CAA55115.1; PID:g463254  
 R;Seow, H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.  
 Immunol. Cell Biol. 72, 398-405, 1994  
 A;Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine interleukin-8.  
 A;Reference number: I46997; MUID:95137691; PMID:7835984  
 A;Accession: I46997  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-101 <SEO>  
 A;Cross-references: UNIPARC:UPI000012D4FE; GB:S74436; NID:g786590; PIDN:AAB33241.1; PID:g786591

C;Genetics:  
A;Gene: IL-8  
C;Superfamily: beta-thromboglobulin  
C;Keywords: chemotaxis; cytokine; inflammation  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-101/Product: interleukin-8 #status predicted <MAT>

Query Match 23.1%; Score 107; DB 2; Length 101;  
Best Local Similarity 30.7%; Pred. No. 6.9e-05;  
Matches 31; Conservative 25; Mismatches 27; Indels 18; Gaps 8;

Qy 1 MNAKVVVVLV---LVLTAALC----LSDGKPVSLSYRCPFRFFESHVARAN---VKHLKIL 50  
| :|: | |: |: ||| || :| || | :| : :| |::  
Db 1 MTSKLAVALLAFLLSAALCEAAVLS---RMSTELRCQC--IKTHSTPFHPKFIKELRVI 55

Qy 51 NT-PNCA-LQIVARLKNNNRQVCIDPKLKWIQEYLEKALNK 89  
: |:| :|: :| | :||:|||| ||:|: :: | :  
Db 56 ESGPHCENSEIIVKL-TNGKEVCLDPKEKWVQKVQAFLKR 95

#### RESULT 13

A28815

monocyte chemoattractant cytokine RANTES precursor - human

N;Alternate names: small inducible cytokine A5; T-cell specific cytokine RANTES

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1989 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

C;Accession: A28815

R;Schall, T.J.; Jongstra, J.; Dyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis, M.M.; Krensky, A.M.

J. Immunol. 141, 1018-1025, 1988

A;Title: A human T cell-specific molecule is a member of a new gene family.

A;Reference number: A28815; MUID:88285659; PMID:2456327

A;Accession: A28815

A;Molecule type: mRNA

A;Residues: 1-91 <SCH>

A;Cross-references: UNIPROT:P13501; UNIPARC:UPI000004A187; GB:M21121

C;Comment: The acronym RANTES reflects the description "Regulated upon Activation, Normal T Expressed, Secreted".

C;Genetics:

A;Gene: GDB:SCYA5; D17S136E

A;Cross-references: GDB:120749; OMIM:187011

A;Map position: 17q11.2-17q12

C;Superfamily: macrophage inflammatory protein

C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-91/Product: T-cell protein RANTES #status predicted <MAT>

Query Match 23.0%; Score 106.5; DB 1; Length 91;  
Best Local Similarity 33.3%; Pred. No. 7.1e-05;  
Matches 27; Conservative 18; Mismatches 29; Indels 7; Gaps 5;

Qy 7 VVLVLTALCL-SDGKPVSLSYRCPFRFFESHVARANVK-HLK--ILNTPNCALQIVAR 62  
: ::|: |||| : | | | || | ::|| : |:| : |: |

Db 8 LAVILIATALCAPASASPYS-SDTTPCCF--AYIARPLPRAHIKEYFYFTSGKCSNPAVVF 64

Qy 63 LKNNNRQVCIDPKLKWIQEYL 83  
: ||||| :|: ||: ||:

## RESULT 14

A46539

monocyte chemoattractant cytokine RANTES precursor - mouse

N;Alternate names: MuRantes

C;Species: Mus musculus (house mouse)

C;Date: 18-Jun-1993 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

C;Accession: I48875; A46539; I48654; I56970

R;Danoff, T.M.; Lalley, P.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.

J. Immunol. 152, 1182-1189, 1994

A;Title: Cloning, genomic organization, and chromosomal localization of the Scya5 gene encoding the murine chemokine RANTES.

A;Reference number: I48875; MUID:94132613; PMID:7507961

A;Accession: I48875

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-91 &lt;DAN&gt;

A;Cross-references: UNIPROT:P30882; UNIPARC:UPI000000028C; EMBL:U02298;

NID:g460090; PIDN:AAA18302.1; PID:g460091

R;Schall, T.J.; Simpson, N.J.; Mak, J.Y.

Eur. J. Immunol. 22, 1477-1481, 1992

A;Title: Molecular cloning and expression of the murine RANTES cytokine: structural and functional conservation between mouse and man.

A;Reference number: A46539; MUID:92289805; PMID:1376260

A;Accession: A46539

A;Molecule type: mRNA

A;Residues: 1-18, 'A', 20-91 &lt;SCH&gt;

A;Cross-references: UNIPARC:UPI0000151811; GB:S37648; NID:g250207;

PIDN:AAB22330.1; PID:g250208

A;Experimental source: macrophage cell line PU5-1.8

A;Note: sequence extracted from NCBI backbone (NCBIN:106768, NCBIP:106770)

R;Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Paznekas, W.A.

Mol. Cell. Biol. 14, 2914-2925, 1994

A;Title: Definition of a lipopolysaccharide-responsive element in the 5'-flanking regions of MuRantes and crg-2.

A;Reference number: I48654; MUID:94217689; PMID:7513046

A;Accession: I48654

A;Status: translation not shown; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-91 &lt;SHI&gt;

A;Cross-references: UNIPARC:UPI000000028C; EMBL:X70675; NID:g475205;

PIDN:CAA50011.1; PID:g475206

R;Neilson, E.G.; Krensky, A.

Kidney Int. 41, 220-225, 1992

A;Title: Isolation and characterization of cDNA from renal tubular epithelium encoding murine Rantes: A small intercrine from the Scy superfamily.

A;Reference number: I56970; MUID:92277990; PMID:1375672

A;Accession: I56970

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-40, 'E', 42-91 &lt;NEI&gt;

A;Cross-references: UNIPARC:UPI000016380F; GB:M77747; NID:g200649;

PIDN:AAA40029.1; PID:g200650

C;Comment: This chemoattractant for monocytes but not neutrophils is an immediate-early response protein to LPS stimulation.  
 C;Genetics:  
 A;Introns: 26/1; 63/2  
 C;Superfamily: macrophage inflammatory protein  
 C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation  
 F;1-23/Domain: signal sequence #status predicted <SIG>  
 F;24-91/Product: monocyte chemoattractant cytokine RANTES #status predicted <MAT>

Query Match 23.0%; Score 106.5; DB 1; Length 91;  
 Best Local Similarity 36.7%; Pred. No. 7.1e-05;  
 Matches 29; Conservative 11; Mismatches 34; Indels 5; Gaps 3;

Qy 9 LVLVLTALCLSDGKPVSL--SYRCPCRFFESHVA--RANVKHLKILNTPNCALQIVARLK 64  
 |::||| | | | || | :| ||:|| : | : | :  
 Db 8 LTIILTAAALCTPAPASPYGSDTTPCCFAYLSLALPRAHVKEY-FYTSSKCSNLAVVFT 66  
 Qy 65 NNNRQVCIDPKLKWIEYL 83  
 ||||| :|: ||:|:|:  
 Db 67 RRNRQVCANPEKKWVQEYI 85

RESULT 15  
 B28414

growth-regulated protein precursor - Chinese hamster  
 C;Species: Cricetulus griseus (Chinese hamster)  
 C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
 C;Accession: B28414  
 R;Anisowicz, A.; Bardwell, L.; Sager, R.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987  
 A;Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese hamster and human cells.  
 A;Reference number: A94184; MUID:88041072; PMID:2890161  
 A;Accession: B28414  
 A;Molecule type: mRNA  
 A;Residues: 1-101 <ANI>  
 A;Cross-references: UNIPROT:P09340; UNIPARC:UPI000012BAF7; GB:J03560;  
 NID:g191088; PIDN:AAA36985.1; PID:g304509  
 A;Note: the authors translated the codon CAG for residue 52 as Glu  
 C;Superfamily: beta-thromboglobulin  
 F;1-23/Domain: signal sequence #status predicted <SIG>  
 F;24-101/Product: growth-regulated protein #status predicted <MAT>

Query Match 23.0%; Score 106.5; DB 2; Length 101;  
 Best Local Similarity 29.8%; Pred. No. 7.8e-05;  
 Matches 25; Conservative 24; Mismatches 32; Indels 3; Gaps 3;

Qy 6 VVVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNT-PNCA-LQIVARL 63  
 ::||:| | : | ||: || | : | |:: ||: | :| ::| |  
 Db 13 LLLLLLLLATSRLATGAPVANELRCQCLQTMGTGVHLKNIQSLKVTPPGPHCTQTEVIATL 72  
 Qy 64 KNNNRQVCIDPKLKWIEYLEKAL 87  
 | | :: |::| :|: ::| |  
 Db 73 K-NGQEACLNPEAPMVQKIVQKML 95

Search completed: April 26, 2006, 02:38:13  
Job time : 39 secs